

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:20:22 ; Search time 17 Seconds

(Without alignments)  
1997.389 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1828  
Sequence: 1 MPWLLLLVAVSGAQTTPC.....KVPILHCVDTRSANRPTLL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database :

1: PIR 78: \*  
2: PIR1: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235	67.6	242	2	T14791
2	279.5	15.3	662	2	S42799
3	265	14.5	907	2	JE0176
4	263	14.4	707	2	UC0763
5	257	14.1	907	2	UC0193
6	247	13.5	560	2	A60164
7	236.5	12.9	312	1	NBHUN2
8	234.5	12.8	605	2	UC5239
9	230.5	12.6	1091	2	A58532
10	225	12.3	1531	2	T42218
11	224.5	12.3	605	2	A41915
12	217	11.9	738	2	T19398
13	215.5	11.8	603	2	JC1282
14	215.5	11.8	1066	2	T15854
15	215	11.8	1389	2	T13852
16	214.5	11.7	603	2	UC6128
17	213	11.6	1385	2	T13887
18	212	11.6	357	2	S24317
19	211.5	11.6	1256	2	S60461
20	210.5	11.5	1523	2	T13953
21	210	11.5	836	2	T46070
22	206	11.3	622	2	TC9793
23	203	11.1	458	2	T19941
24	203	11.1	575	2	T29972
25	201.5	11.0	526	2	C84552
26	201.5	11.0	680	2	T19939
27	201	11.0	961	2	T23395
28	199	10.9	1119	2	AD1822
29	198	10.8	354	2	S29145

30	197	10.8	536	2	A34901	lysine carboxypept
31	197	10.8	1134	1	A29944	chaoprin precursor
32	195.5	10.7	360	2	S06280	decorin precursor
33	195.5	10.7	360	2	I47020	decorin - rabbit
34	194.5	10.6	354	2	A55454	decorin precursor
35	194	10.6	1051	2	T13174	gpi10 protein - fr
36	193.5	10.6	342	2	A46743	lumican precursor
37	192	10.6	1778	2	AF1116	internalin protein
38	190.5	10.4	359	1	NBHUC8	decorin precursor
39	189.5	10.4	369	2	S32559	biglycan precursor
40	183.5	10.0	338	2	S52284	lumicon, secretory
41	183.5	10.0	369	2	S20811	proteoglycan I - m
42	183.5	10.0	369	2	S32793	biglycan precursor
43	183.5	10.0	424	2	S27783	hypothetical prote
44	181.5	9.9	343	2	A41748	human precursor
45	181.5	9.9	1257	2	A68536	protein B0523.5 [i
46	181	9.9	496	2	C96832	hypothetical prote
47	181	9.9	789	2	T28714	hypothetical prote
48	181	9.9	1355	2	T28715	hypothetical prote
49	180.5	9.9	440	2	A47530	oligodendrocyte-my
50	180	9.8	368	1	BGHUN	biglycan precursor
51	179.5	9.8	440	2	A39613	oligodendrocyte-my
52	179.5	9.8	1469	2	B36655	slit protein 2 pre
53	179.5	9.8	1480	2	A36655	slit protein 1 pre
54	179	9.8	1039	2	T22117	hypothetical prote
55	176.5	9.8	1268	2	A49674	flightsless-1 homol
56	176.5	9.7	1112	2	T10504	disease resistance
57	176	9.6	653	2	T25194	hypothetical prote
58	176	9.6	864	2	T08575	protein kinase hom
59	175	9.5	858	2	T00258	hypothetical prote
60	174	9.5	462	2	D84858	hypothetical prote
61	172.5	9.4	404	2	T08549	hypothetical prote
62	172	9.4	361	2	A53860	chondroadherin pre
63	171.5	9.4	626	1	NBHUIA	platelet glycoprot
64	171.5	9.4	682	2	A49121	cell-surface molec
65	171.5	9.4	682	2	A43318	connectin precursor
66	171	9.4	375	2	S05390	fibronectin precu
67	171	9.4	376	2	S55275	fibronectin precu
68	170.5	9.3	1143	2	T10636	hypothetical prote
69	169	9.2	964	2	T49038	hypothetical prote
70	168	9.2	395	2	T01392	leucine-rich repea
71	167	9.1	603	2	T24315	hypothetical prote
72	167	9.1	851	2	S67285	NMD1 protein - yea
73	167	9.1	855	2	T17460	disease resistance
74	166.5	9.1	562	2	T34319	hypothetical prote
75	166.5	9.1	567	2	T46210	hypothetical prote
76	165.5	9.1	1115	2	S40241	G protein-coupled
77	165	9.0	1143	2	B84431	probable receptor
78	165	9.0	1535	2	S46224	peroxylasein - fru
79	165	9.0	2493	2	A55481	adenylate cyclase
80	164.5	9.0	549	2	T41744	hypothetical prote
81	164.5	9.0	679	2	T20713	hypothetical prote
82	164	9.0	420	2	A53531	oncofetal tropobol
83	164	9.0	740	2	B84741	hypothetical prote
84	163	8.9	1025	2	T42626	secreted leucine-r
85	163	8.9	1839	1	OYBYK	adenylate cyclase
86	162	8.9	2026	1	OYBYK	adenylate cyclase
87	160	8.8	528	2	T15198	hypothetical prote
88	160	8.8	1134	2	T04587	hypothetical prote
89	159.5	8.7	559	2	T42998	Ras-binding protei
90	159	8.7	382	2	T13068	proline- arginine-
91	158.5	8.7	478	2	H86459	hypothetical prote
92	158.5	8.7	480	2	TC00971	probable disease r
93	158.5	8.7	809	2	B84631	probable receptor-
94	158	8.6	768	2	T17462	disease resistance
95	158	8.6	1097	2	A29943	Toll protein precu
96	158	8.6	1192	2	T48499	receptor-like prot
97	157	8.6	661	2	I56258	RPI05 - mouse
98	157	8.6	1025	1	A57676	protein kinase Xa2
99	156.5	8.6	572	2	T30947	hypothetical prote
100	156.5	8.6	613	2	A88684	protein AC7.2 (lmp
101	156.5	8.6	863	2	A55173	cf-9 protein precu
102	155.5	8.5	380	2	S71876	fibronectin - chi

103	154.5	8.5	976	2	B84659	probable receptor-
104	154	8.4	720	2	T02361	hypothetical prote
105	154	8.4	890	2	T00800	disease resistance
106	153.5	8.4	771	2	T02565	disease resistance
107	153.5	8.4	994	2	H96510	probable disease r
108	153	8.4	538	2	T01102	disease resistance
109	153	8.4	800	2	G84740	hypothetical prote
110	153	8.4	925	2	G84538	probable LRR recep
111	153	8.4	1027	2	B85089	receptor protein k
112	152.5	8.3	224	2	T32185	hypothetical prote
113	152.5	8.3	540	2	T12704	leucine-rich prote
114	152	8.3	612	2	T10727	protein kinase Xa2
115	151.5	8.3	905	2	T00475	probable disease r
116	151.5	8.3	1338	2	T23007	hypothetical prote
117	151	8.3	380	2	T01281	probable leucine-r
118	151	8.3	855	2	T07015	Cf-4A protein - to
119	150.5	8.2	683	2	T24486	hypothetical prote
120	150.5	8.2	1002	2	T46033	receptor protein k
121	150	8.2	326	2	T24722	hypothetical prote
122	149.5	8.2	432	2	F86263	hypothetical prote
123	149.5	8.2	980	2	H84632	probable receptor-
124	149	8.2	335	2	H84616	protein F21B7.6 f1
125	149	8.2	397	2	T00914	leucine-rich repa
126	147	8.0	382	2	T04260	hypothetical prote
127	147	8.0	800	2	S37387	internalin A (limp
128	147	8.0	800	2	AB1129	internalin A (limp
129	147	8.0	1029	2	T00712	protein kinase hom
130	147	8.0	1068	2	H96769	hypothetical prote
131	147	8.0	1784	2	G96615	hypothetical prote
132	146.5	8.0	717	2	T33395	hypothetical prote
133	146.5	8.0	996	2	F86410	protein F3M18.12 f
134	146.5	8.0	1232	2	T05322	hypothetical prote
135	146	8.0	554	2	T23841	hypothetical prote
136	146	8.0	830	2	B84846	probable receptor-
137	145.5	8.0	332	2	H84527	hypothetical prote
138	145.5	8.0	677	2	H86208	protein F2G5.26 f
139	145	7.9	448	2	T27395	hypothetical prote
140	145	7.9	1029	2	T05050	protein kinase hom
141	145	7.9	1196	2	T09356	brassinosteroid-in
142	144.5	7.9	1025	2	T45647	monocyte surface g
143	144.5	7.9	960	2	G84652	receptor protein k
144	143.5	7.8	298	2	UC4130	probable receptor-
145	143	7.8	596	2	AE1515	osteoglycin precu
146	143	7.8	818	2	T01105	internalin like pr
147	143	7.8	907	2	A86460	disease resistance
148	143	7.8	702	2	T21148	99.9K hypothetical
149	142.5	7.8	981	2	T50651	hypothetical prote
150	142.5	7.8	2145	2	UC4747	receptor protein k
151	142	7.8	864	2	D84740	adenylate cyclase
152	142	7.8	1692	2	A33988	hypothetical prote
153	141.5	7.7	800	2	H84740	hypothetical prote
154	141	7.7	869	2	A71400	probable disease r
155	140.5	7.7	1120	2	B64799	hypothetical prote
156	140.5	7.7	987	2	T50860	receptor protein k
157	140	7.7	610	2	T23836	hypothetical prote
158	139	7.6	818	2	F96586	hypothetical prote
159	138.5	7.6	1019	2	G96519	probable disease r
160	138.5	7.5	322	2	S72271	proteoglycan lb pr
161	138	7.5	485	2	B86460	hypothetical prote
162	138	7.5	932	2	T48489	receptor-like prote
163	138	7.5	988	2	T45717	receptor-kinase 11
164	138	7.5	1088	2	E86312	filike.9 protein -
165	137.5	7.5	598	2	G96756	receptor-like prot
166	137.5	7.5	853	2	AG0123	probable antigenic
167	137.5	7.5	605	2	T17461	disease resistance
168	137.5	7.5	835	2	G84648	probable disease r
169	137.5	7.5	1152	2	T31911	hypothetical prote
170	137	7.5	409	2	T43589	Yop targeted effec
171	137	7.5	499	2	S49301	AMU1175 protein -
172	136.5	7.5	397	2	T49292	hypothetical prote
173	136.5	7.5	505	2	AC1469	internalin like pr
174	136.5	7.5	845	2	T07039	Hox9-0 protein - t
175	136.5	7.5				

176	136.5	7.5	1109	2	T18535	receptor-like prot
177	136.5	7.5	1166	2	F96598	protein F20N2.4 f1
178	136	7.5	983	2	G84524	probable disease r
179	136	7.4	999	1	S27756	receptor-like prote
180	136	7.4	1123	2	D96756	receptor-like prote
181	135.5	7.4	766	2	T01817	hypothetical prote
182	135.5	7.4	992	2	T05335	hypothetical prote
183	135.5	7.4	1016	2	T30653	disease resistance
184	135	7.4	316	2	A41781	proteoglycan-lb -
185	135	7.4	371	2	T49908	hypothetical prote
186	135	7.4	962	2	T04124	receptor-like prote
187	135	7.4	1133	2	E86308	AMU1218 protein -
188	134.5	7.4	500	2	S49302	hypothetical prote
189	134.5	7.4	568	2	F86291	hypothetical prote
190	134	7.3	421	2	T46266	probable receptor-
191	134	7.3	1007	2	G84568	protein kinase Xa2
192	133.5	7.3	996	2	T10725	probable receptor-
193	133.5	7.3	1124	2	B84742	hypothetical prote
194	133	7.3	391	2	T04609	protein kinase Xa2
195	133	7.3	499	2	D83333	hypothetical prote
196	133	7.3	813	2	T04313	hypothetical prote
197	133	7.3	889	2	T20123	hypothetical prote
198	132.5	7.2	910	2	G02020	p37NB - human
199	132	7.2	313	2	UC7361	foliilitropin recept
200	132	7.2	696	2	G84524	probable disease r
201	132	7.2	1011	2	A38971	polycystic kidney
202	132	7.2	4302	2	T46170	disease resistance
203	131.5	7.2	904	2	T46170	hypothetical prote
204	131	7.2	305	2	T46721	ipah protein - Shi
205	131	7.2	574	2	T05887	protein kinase hom
206	131	7.2	976	2	T05888	hypothetical prote
207	131	7.2	1003	2	T05888	tsu-1 homolog - hu
208	130.5	7.1	277	2	G86459	Hypothetical 55.6
209	129.5	7.1	342	2	S23764	polygalacturonase-
210	129.5	7.1	419	2	A90888	hypothetical prote
211	129.5	7.1	419	2	H85729	hypothetical prote
212	129.5	7.1	613	2	T15489	hypothetical prote
213	129.5	7.1	890	2	C96654	hypothetical prote
214	129.5	7.1	1013	2	T10659	probable serine/th
215	129.5	7.1	277	2	S25770	RSP-1 protein - mo
216	129	7.1	277	2	E88451	protein X10D2.1 f1
217	129	7.1	1223	2	B86234	hypothetical prote
218	128.5	7.0	921	2	B86455	hypothetical prote
219	128.5	7.0	1064	2	C84517	probable receptor-
220	128	7.0	886	2	G96772	probable antigenic
221	128	7.0	626	2	AE0123	hypothetical prote
222	127.5	7.0	719	2	T47727	osteoinductive fac
223	127	7.0	298	2	B35272	probable disease r
224	127	6.9	835	2	T05259	hypothetical prote
225	127	6.9	1008	2	T13476	probable antigenic
226	127	6.9	1286	2	AF0123	hypothetical prote
227	127	6.9	291	2	T34555	osteoinductive fac
228	126.5	6.9	333	2	A35272	hypothetical prote
229	126.5	6.9	299	2	T08903	hypothetical prote
230	126	6.9	364	2	T08903	similar to disease
231	126	6.9	729	2	F86308	hypothetical prote
232	126	6.9	977	2	G96745	hypothetical prote
233	126	6.9	1131	2	F86662	hypothetical prote
234	126	6.9	311	2	B86211	hypothetical prote
235	125.5	6.9	621	2	T39204	probable LRR recep
236	125.5	6.9	767	2	B84594	G protein-coupled
237	125.5	6.9	925	2	UC2033	hypothetical prote
238	125.5	6.9	925	2	T04868	probable disease r
239	125	6.8	431	2	T05250	protein kinase hom
240	125	6.8	980	2	T05414	receptor-kinase li
241	125	6.8	1011	2	T45718	suppressor protein
242	125	6.8	338	2	G38030	internalin, probab
243	124.5	6.8	666	2	A11174	probable disease r
244	124.5	6.8	668	2	T05257	hypothetical prote
245	124.5	6.8	849	2	C97303	internalin, probab
246	124.5	6.8	851	2	AD1437	
247	124.5	6.8	860	2	S68205	
248	124	6.8	360	2		

249	124	6.8	473	2	D85041	hypothetical prote	322	111	6.1	612	2	I73633	gene txc protein
250	123.5	6.8	670	2	H96707	probable receptor	323	111	6.1	601	2	C85282	hypothetical prote
251	123	6.7	218	2	T01104	disease resistance	324	111	6.1	767	2	T28418	ORF MSV257 leucine
252	123	6.7	432	2	B96712	unknown protein, 6	325	111	6.1	825	2	A55178	neurotrophin recep
253	123	6.7	728	2	D86278	hypothetical prote	326	111	6.1	835	2	I73632	neurotrophin-3-rec
254	123	6.7	1045	2	T41119	internalin - relate	327	111	6.1	943	1	E84429	probable receptor-
255	122.5	6.7	630	2	S13724	ESAG 8 protein - T	328	110.5	6.0	494	2	B96534	hypothetical prote
256	122.5	6.7	743	2	C84633	probable disease r	329	110.5	6.0	695	2	I45896	follicle stimulat
257	122	6.7	268	2	T19697	hypothetical prote	330	110.5	6.0	855	2	T05981	hypothetical prote
258	122	6.7	367	2	A33950	YopM protein - Yex	331	110.5	6.0	874	2	E97302	hypothetical prote
259	122	6.7	990	2	T03784	probable receptor	332	110.5	6.0	984	2	T48216	hypothetical prote
260	121.5	6.6	391	2	S49300	AMU1236 protein -	333	110	6.0	573	2	A85357	receptor-like kina
261	121.5	6.6	674	2	S59476	kinase-like transm	334	110	6.0	646	2	B84852	probable receptor-
262	121	6.6	808	2	B97303	hypothetical prote	335	110	6.0	699	2	T15920	hypothetical prote
263	121	6.6	1495	2	T31434	denisin-180 - rat	336	110	6.0	1337	2	AC1583	internalin protein
264	120.5	6.6	329	2	T17033	leucine rich repea	337	109.5	6.0	388	2	AF1383	internalin protein
265	120.5	6.6	630	2	A36359	VSG expression sit	338	109.5	6.0	947	2	G86420	probable receptor-
266	120.5	6.6	951	2	A96770	hypothetical prote	339	109.5	6.0	1731	2	AB3045	ice nucleation pro
267	120	6.6	694	2	UC2237	foliitropin recept	340	109.5	6.0	1731	2	B96241	hypothetical prote
268	119.5	6.5	191	2	E84740	hypothetical prote	341	109.5	6.0	2327	2	T42630	aggreccan - bovine
269	119.5	6.5	567	2	H84770	probable receptor-	342	109	6.0	735	2	T00850	probable receptor-
270	119.5	6.5	581	2	G96811	unknown protein T1	343	109	6.0	764	2	A40077	thyrotropin recept
271	119.5	6.5	607	2	C84630	probable LRR recep	344	109	6.0	978	2	E96787	receptor kinase-1i
272	119.5	6.5	991	2	T52400	receptor-like prot	345	109	6.0	1009	2	T45645	hypothetical prote
273	118.5	6.5	699	2	T05225	extensin homolog F	346	109	6.0	1095	2	G96746	hypothetical prote
274	118.5	6.5	766	2	G86308	similar to disease	347	108.5	5.9	173	2	T47176	hypothetical prote
275	118	6.5	349	2	T15422	hypothetical prote	348	108.5	5.9	474	1	C39667	brain-derived neur
276	117.5	6.4	176	1	A46606	platelet glycoprot	349	108.5	5.9	476	1	B39667	brain-derived neur
277	117.5	6.4	383	2	B86272	protein F16A1.12	350	108.5	5.9	654	2	C87587	hypothetical prote
278	117.5	6.4	656	2	AE1479	receptor-cell surf	351	108.5	5.9	821	1	A39667	hypothetical prote
279	117.5	6.4	662	2	T46005	receptor-like prot	352	108.5	5.9	839	2	T04859	brain-derived neur
280	117	6.4	885	2	B86257	NBS/LRR disease re	353	108.5	5.9	967	2	G96637	extensin homolog F
281	116.5	6.4	945	2	T05251	probable disease re	354	108	5.9	764	2	I48882	hypothetical prote
282	116.5	6.4	1234	2	T14515	hypothetical prote	355	108	5.9	920	2	F86420	probable receptor-
283	115.5	6.3	318	2	B64900	hypothetical prote	356	107.5	5.9	389	2	H86266	hypothetical prote
284	115.5	6.3	327	2	T10263	probable polygalac	357	107.5	5.9	902	2	T00588	hypothetical prote
285	115.5	6.3	548	2	AH1107	internalin H limpo	358	107	5.9	407	2	S36779	ribosome-binding p
286	115.5	6.3	671	2	D84648	probable disease r	359	107	5.9	467	2	G83266	cytochrome c P433
287	115.5	6.3	695	2	UC1493	foliitropin recept	360	107	5.9	499	2	H87460	hypothetical prote
288	115.5	6.3	716	2	H84421	probable receptor-	361	107	5.9	618	2	T48193	hypothetical prote
289	115.5	6.3	942	1	UC1674	protein kinase TMK	362	107	5.9	1121	2	A82809	exodeoxyribonuclea
290	115.5	6.3	1109	2	C84545	probable disease r	363	107	5.9	2944	2	A54849	collagen alpha 1(V
291	115	6.3	940	2	H86420	probable receptor-	364	106.5	5.8	670	2	T00083	hypothetical prote
292	115	6.3	985	2	T06049	hypothetical prote	365	106.5	5.8	886	2	T40734	probable adenylate
293	114.5	6.3	756	2	C87432	hypothetical prote	366	106	5.8	499	2	AT1107	internalin E limpo
294	114.5	6.3	1112	2	T00992	hypothetical prote	367	106	5.8	521	2	AC1949	hypothetical prote
295	114.5	6.3	1219	2	T06608	disease resistance	368	106	5.8	2062	2	G96602	probable receptor
296	114	6.2	327	2	S47965	polylacturonase	369	105.5	5.8	719	2	F96577	hypothetical prote
297	114	6.2	366	1	TDM5M4	monocyte surface g	370	105.5	5.8	760	2	T06291	extensin homolog T
298	114	6.2	966	2	D96662	hypothetical prote	371	105.5	5.8	919	2	T05746	hypothetical prote
299	114	6.2	2224	1	KFHU5	coagulation factor	372	105.5	5.8	921	2	D86293	F7H2.22 protein -
300	113.5	6.2	786	2	T01456	extensin homolog F	373	105.5	5.8	942	2	C96574	hypothetical prote
301	113.5	6.2	830	2	C86181	hypothetical prote	374	105	5.7	332	2	C94988	protein phosphatas
302	113.5	6.2	833	2	B85035	hypothetical prote	375	105	5.7	587	2	AC1510	internalin protein
303	113	6.2	518	2	S50465	PAC2 protein - yea	376	105	5.7	673	2	AF1143	internalin protein
304	113	6.2	692	2	A34548	foliitropin recept	377	105	5.7	895	1	JN0898	foliitropin recept
305	113	6.2	1240	2	T06404	resistance complex	378	105	5.7	692	2	T08973	probable serine/th
306	112.5	6.2	630	1	BMUT8Q	regulatory protein	379	104.5	5.7	744	2	E86255	hypothetical prote
307	112.5	6.2	702	2	A86383	76 kD protein kina	380	104.5	5.7	764	2	A35956	thyrotropin recept
308	112.5	6.2	1340	2	A39988	proteoglycan core	381	104.5	5.7	788	2	AC0786	secreted effector
309	112	6.1	589	2	AB1151	internalin protein	382	104.5	5.7	1021	2	AB6421	receptor-like seri
310	112	6.1	660	2	T45569	receptor protein K	383	104	5.7	419	2	A40728	microphthalmia-ass
311	112	6.1	773	2	T00502	probable receptor-	384	104	5.7	695	1	QRHUF	foliitropin recept
312	112	6.1	786	2	T08664	Toll protein-like	385	103.5	5.7	330	2	UC2262	Polylacturonase
313	112	6.1	821	2	AB1126	internalin, peptid	386	103.5	5.7	352	2	S49299	probable disease r
314	111.5	6.1	361	2	AH1469	internalin protei	387	103.5	5.7	509	2	T05260	hypothetical prote
315	111.5	6.1	431	2	T27904	hypothetical prote	388	103.5	5.7	538	2	T47624	hypothetical prote
316	111.5	6.1	449	2	C85332	hypothetical prote	389	103.5	5.7	589	2	T18239	transcription elfe
317	111.5	6.1	449	2	T10650	hypothetical prote	390	103.5	5.7	598	2	AB1236	internalin protein
318	111.5	6.1	825	2	A40026	neurotrophin-3-rec	391	103.5	5.7	617	2	S52797	multi protein - hum
319	111	6.1	227	2	T27905	hypothetical prote	392	103.5	5.7	847	2	F96531	hypothetical prote
320	111	6.1	414	2	C96770	hypothetical prote	393	103	5.6	419	2	I38024	MIRF protein - hum
321	111	6.1	547	2	T09912	hypothetical prote	394	103	5.6	1253	2	T45787	disease resistance

395	103	5.6	2479	2	P87386	conserved hypother
396	102.5	5.6	395	2	A46260	DSP100 protein pre
397	102.5	5.6	630	2	T31798	hypothetical prote
398	102.5	5.6	725	2	T01268	leucine-rich repa
399	102.5	5.6	727	2	C84534	hypothetical prote
400	102.5	5.6	766	2	B85440	receptor kinase-11
401	102	5.6	235	2	S15655	zein, 19K - maize
402	102	5.6	358	2	T01296	leucine-rich repa
403	102	5.6	411	2	AF2320	hypothetical prote
404	102	5.6	744	2	C84527	probable receptor-
405	102	5.6	774	2	D83208	probable ferredoxi
406	102	5.6	783	2	T45889	receptor protein X
407	102	5.6	860	2	C86203	hypothetical prote
408	102	5.6	941	2	B96553	hypothetical prote
409	102	5.6	1063	2	E96662	hypothetical prote
410	102	5.6	1749	2	S75071	hypothetical prote
411	101.5	5.6	296	2	AB1298	internalin C (lipo
412	101.5	5.6	419	2	H96695	hypothetical prote
413	101.5	5.6	852	2	T51259	tyrosine kinase C
414	101.5	5.6	979	2	D86574	hypothetical prote
415	101.5	5.6	1063	2	D86731	hypothetical prote
416	101	5.5	694	2	JC4301	foliitropin recept
417	101	5.5	925	2	H96638	protein TIF9.20 [l
418	101	5.5	1095	2	T01916	hypothetical prote
419	101	5.5	1174	2	T08196	hypothetical prote
420	100.5	5.5	268	2	T45616	hypothetical prote
421	100.5	5.5	638	2	T05606	protein kinase hom
422	100	5.5	787	2	T27632	hypothetical prote
423	100	5.5	794	2	T27633	hypothetical prote
424	100	5.5	868	2	A88860	protein ZC518.3 [l
425	99.5	5.4	367	2	AC1388	internalin protein X
426	99.5	5.4	590	2	B86440	leucine-rich repa
427	99.5	5.4	684	2	T01267	hypothetical prote
428	99.5	5.4	797	2	T26207	hypothetical prote
429	99.5	5.4	892	2	T01899	disease resistance
430	99	5.4	187	2	T26726	hypothetical prote
431	99	5.4	435	2	I39171	cyclin A/CDX2-asso
432	99	5.4	858	2	E96602	hypothetical prote
433	99	5.4	1144	2	A54810	TMV resistance pro
434	99	5.4	1447	2	T42628	neuronal apoptosis
435	98.5	5.4	719	2	T07079	leucine-rich repa
436	98.5	5.4	898	2	P96637	hypothetical prote
437	98.5	5.4	898	2	E96637	hypothetical prote
438	98.5	5.4	898	2	E96637	hypothetical prote
439	98.5	5.4	1171	2	T12956	hypothetical prote
440	98	5.4	415	2	T13435	brain-derived neur
441	98	5.4	476	1	A35104	neurotrophin-3 rec
442	98	5.4	525	1	A58674	neurotrophin-3 rec
443	98	5.4	764	2	JC5643	thyroid stimulat
444	98	5.4	793	2	JC7390	neurotrophin-3 rec
445	98	5.4	803	1	S15695	hypothetical prote
446	98	5.4	821	1	S06943	brain-derived neur
447	98	5.4	1405	2	T04426	hypothetical prote
448	97.5	5.3	811	2	T48468	disease resistance
449	97.5	5.3	857	2	S44893	ice nucleation pro
450	97.5	5.3	951	2	T03511	probable disease r
451	97.5	5.3	957	2	E84547	hypothetical prote
452	97.5	5.3	1029	2	E96602	disease resistance
453	97.5	5.3	1217	2	T52348	hypothetical prote
454	97.5	5.3	2117	2	T36180	CDA peptide synthe
455	97	5.3	176	2	T23475	hypothetical prote
456	97	5.3	252	2	T01787	thyrotropin recept
457	97	5.3	253	2	JC1319	thyrotropin recept
458	97	5.3	343	2	G75381	hypothetical prote
459	97	5.3	381	2	S59943	early nodulin 8 pr
460	97	5.3	456	2	A31857	ribonuclease inhib
461	97	5.3	533	2	T52063	ran GTPase-activat
462	97	5.3	601	2	H96740	hypothetical prote
463	97	5.3	750	2	D86245	hypothetical prote
464	97	5.3	764	1	QRH0R8	thyrotropin recept
465	97	5.3	851	2	H84455	probable receptor-
466	97	5.3	2149	2	C96695	ribulose biphosph
467	96.5	5.3	343	2	C69019	conserved hypother

468	96.5	5.3	452	2	T46147	zinc finger protei
469	96.5	5.3	530	2	B37471	capid protein - N
470	96.5	5.3	532	2	A35149	ipah protein - Shi
471	96.5	5.3	647	2	T05585	hypothetical prote
472	96.5	5.3	688	2	T04568	protein kinase hom
473	96.5	5.3	940	2	AB1744	internalin protein
474	96.5	5.3	1715	2	T06145	disease resistance
475	96	5.3	263	1	Z1ZM21	22K zein precursor
476	96	5.3	266	2	B22831	22K zein precursor
477	96	5.3	500	2	D92302	hypothetical prote
478	96	5.3	934	2	T05201	hypothetical prote
479	96	5.3	1036	2	E96682	hypothetical prote
480	96	5.3	1179	2	T04584	TMV resistance pro
481	95.5	5.2	630	2	AC1129	zinc finger/leucin
482	95.5	5.2	1027	2	I38759	DNA polymerase III
483	95	5.2	387	2	AD2057	probable transfera
484	95	5.2	388	2	B70878	brain-derived neur
485	95	5.2	427	1	T73631	brain-derived neur
486	95	5.2	520	1	S44099	brain-derived neur
487	95	5.2	593	1	X1Z7FG	brain-derived neur
488	95	5.2	672	2	B84782	probable receptor-
489	95	5.2	799	1	BVKW21	zyg1 protein - Ca
490	95	5.2	818	1	S44098	brain-derived neur
491	95	5.2	822	1	A56853	brain-derived neur
492	95	5.2	1294	2	T18546	flax rust resist
493	95	5.2	6420	2	T30283	polyketide synthas
494	94.5	5.2	174	2	S43889	AKU3 protein - wh
495	94.5	5.2	511	2	T43282	alip1 protein - fi
496	94.5	5.2	833	2	H96651	protein T3P18.19 [
497	94.5	5.2	956	2	T52414	H+-exporting ATPas
498	94.5	5.2	1007	2	T47430	disease resistance
499	94.5	5.2	1093	2	I38533	AF17 protein - hum
500	94.5	5.2	1590	2	B86398	protein TTN9.24 [l

## ALIGNMENTS

RESULT 1  
T14791  
hypothetical protein DKFZP586E011.1 - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 20-Sep-1999 #Sequence, revision 20-Sep-1999 #next\_change 20-Sep-1999

C/Accession: T14791  
R/Koshier, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999  
A/Reference number: Z18180

A/Accession: T14791  
A/Status: preliminary

A/Residues: 1-242 <KOB>  
A/Cross-References: EMBL:AL10276

A/Experimental source: adult uterus; clone DKFZP586E011  
C/Genetics:

A/Note: DKFZP586E011.1

Query March 67.6%; Score 1235; DB 2; Length 242;  
Best Local Similarity 99.6%; Pred. No. 2, 2e-89;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	112	SDLSHNGLTALPAESFTSSPLSDVNLSHNQREVSAFTTHSGRALHVDLSHNLIR	171
DB	1	SDLSHNGLTALPAESFTSSPLSDVNLSHNQREVSAFTTHSGRALHVDLSHNLIR	60
QY	172	LVHPFRAGAPATTISLNNRRHAYVNNRDLPLRTLSIDGNPLAVTGGAPAGGL	231
DB	61	LVHPFRAGAPATTISLNNRRHAYVNNRDLPLRTLSIDGNPLAVTGGAPAGGL	120
QY	232	THLSIASLQRLPELAPSGFRELPGIQVLDLSGNPKLNAGAEEVSGSLIQELDLSGNTL	291
DB	121	THLSIASLQRLPELAPSGFRELPGIQVLDLSGNPKLNAGAEEVSGSLIQELDLSGNTL	180
QY	292	VPLPEALLHLHPALQSVSVGQVRCRRLVREGTYRRRGSSPKVPLHCVDRBSAAGPT	351

Db 181 VPEALLLHPALQSVGVQDVRCRRLVREGTYPRRPGSSPVVALHCVTRRESARGP 240  
 QY 352 IL 353  
 Db 241 IL 242

## RESULT 2

garp precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jul-2000  
 C:Accession: S42799; I37407

R:Birdnam, D.  
 submitted to the EMBL Data Library, July 1993

A:Reference number: S42799  
 A:Accession: S42799

A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-662 <BIR>  
 R:Ollendorff, V.; Noguchi, T.; deJareyriere, O.; Birdnam, D.  
 Cell Growth Differ. 5, 213-219, 1994

A:Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain

A:Reference number: I37407; MUID:94235567; PMID:8180135

A:Accession: I37407  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-662 <RBS>

A:Cross-references: RBS>  
 A:Gene: GDB:GARP; D11S833E

A:Map position: 11q13.5-11q14  
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
 F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>  
 F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>  
 F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>  
 F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>  
 F:340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:384-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>  
 F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>  
 F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>  
 F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>  
 F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

Query Match 15.3%; Score 279.5; DB 2; Length 662;  
 Best Local Similarity 28.8%; Pred. No. 5.8e-14;

Matches 126; Conservative 47; Mismatches 113; Indels 151; Gaps 20;

QY 5 LLLLLAV-----GGAOTTRPCPFQCCQEVETFGLPFSFSLTRVDCSGGLGHIMVPIPL 58  
 Db 5 LLLLLALITGLAAHQKQKVC-----KMDK-----KSCQVGLGLQVPSVLP 49  
 QY 59 DTAHLIDSSNRLKEMNBSVLGP--GYTTAGLDLSHNLTSISPTAFSRRLRYESLDLS 116  
 Db 50 DTEILDLSGNQL-----RSILASPLGFYALRHLDLSTWETSFLQPGAFQALHLEHSLA 105  
 QY 117 HNGI---TALPAESFTSSP-LSDVNLISHNOLREVSVSAFTTHSGGRLAHVDLSHNLHRL 172  
 Db 106 HRLAMATLASNGIGLPLRVTSLDLSGNSLYS-----GLERL 144  
 QY 173 VPHPTAGLPAPFTIOSLNLAMNRLHAYP--NLRLDP--LRYSLDGNPLAVIGGAFAGLG 229

Db 145 LGE-----APSLHTLSAENSILRLTRHFRFVPALEQDLHNSVMDLEDGAFELP 197  
 QY 230 GLTHLSLA-----SLQRL  
 Db 198 RLTHNLISNNSLVTICISDFSLQQLRVLDLSGNSIEAFQASQPAEQFQTLWDLRENKLIH 257  
 QY 243 -PELAPSGFRELPGLQVLDLGN-----PLTNAGAEV-----PSG- 277  
 Db 258 FPDLA-----ALPRLIYNLSNNLRLPTGPQDSKGTHAPSEGSALPLAPSGNASGR 312  
 QY 278 -LSSIQEIDLSGNTLVPIPEALLLHPALQSVGVQDVRCRRLVREGTYPRRPGSSPKVP 336  
 Db 313 PLISQLINDLSVNEIELPDSFLHRLTSLCFNLERN--CLRTFE-----ARLGLSLPCLM 366  
 QY 337 L-----HCVDTRRESAAR 348  
 Db 367 LLDLSHNALELDELGAR 383

## RESULT 3

JB0176  
 orphan G protein-coupled receptor precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 21-Jul-2000

C:Accession: JB0176  
 R:McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q.

Biochem. Biophys. Res. Commun. 247, 266-270, 1998  
 A:Title: Identification and cloning of an orphan G protein-coupled receptor of the glyc

A:Reference number: JB0176; MUID:98308104; PMID:9642114

A:Accession: JB0176  
 A:Molecule type: mRNA

A:Residues: 1-907 <MCDD>  
 A:Cross-references: GB:AF062006; NID:93366801; PIDN:AAC28019.1; PID:93366802

C:Comment: This protein is a receptor for a novel class of glycoprotein ligands.  
 C:Gene: HG38

A:Map position: 12q22-23  
 F:1-21/Domain: signal sequence #status predicted <SIG>

F:562-583/Domain: transmembrane #status predicted <TM1>  
 F:594-616/Domain: transmembrane #status predicted <TM2>

F:639-660/Domain: transmembrane #status predicted <TM3>  
 F:681-701/Domain: transmembrane #status predicted <TM4>

F:725-744/Domain: transmembrane #status predicted <TM5>  
 F:768-791/Domain: transmembrane #status predicted <TM6>

F:803-824/Domain: transmembrane #status predicted <TM7>

Query Match 14.5%; Score 265; DB 2; Length 907;  
 Best Local Similarity 30.1%; Pred. No. 1.2e-12;

Matches 93; Conservative 32; Mismatches 102; Indels 82; Gaps 9;

QY 4 PLLLLAVSQAQ-----TTRPCPFQCCQEVETFGLPFSFSLTRVDCSGGLGHIMVPIPL 58  
 Db 13 PVLQLATGSSPPRSGLVLRGCPTHCHCP-----DGRMLRVVCSDDGSELPSNLSV 66  
 QY 59 DTAHLIDSSNRLKEMNBSVLGP--GYTTAGLDLSHNLTSISPTAFSRRLRYESLDLSH 118  
 Db 67 FTSYLDLSMN-----ISQLPNPLPSIRFLEELRAGN 100  
 QY 119 GLTALPAESFTS--SPISDVNLISHNOLREVSVSAFTTHSGGRLAHVDLSHNLHRLVPHPT 177  
 Db 101 ALTYIPKGAFTGLVSLKVLMLQNNQRLHV-----PT 131  
 QY 178 RAGLPAPFTIOSLNLAMNRLHAYPNLRDL-----LRYSLDGNPLAVIGGAFAGLG 229  
 Db 132 EALQNIQSQSLRLDNHISYVP-----PSGSGLSLHRLWLDVALTEIVQAFRLS 186  
 QY 230 GLTHLSLAQRLPELAPSGFRELPGLQVLDLGNPKNLMAAGAEVPSGSLSQEIDLSGT 289  
 Db 187 ALQAMTLA-LINKIHHPDVAFGNLSGLVYLHNN--RHSLSKKCKGDSHLSLETLDLNN 244  
 QY 290 NLVPLPEAL 298

Db 245 NIDDEPTAI 253

# RESULT 4

UC7763

neural leucine-rich repeat protein-3 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C/Accession: UC7763

R/Fukushima, K.; Matsuo, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.

Biochem. Biophys. Res. Commun. 287, 257-263, 2001

A/Title: Rat neural leucine-rich repeat protein-3: Cloning and regulation of the gene

A/Reference number: UC7763; PMID:11549284

A/Contents: Fibrosarcoma cells

A/Accession: UC7763

A/Molecule type: mRNA

A/Residues: 1-707 <FUK>

A/Cross-references: GB:AF291437

C/Comment: This protein, a new member of the neural leucine-rich repeat protein family in protein-protein interaction and functions as a cell adhesion molecule or soluble ligand

C/Genetics:

A/Genes: nlrr-3

C/Keywords: cell adhesion

Query Match 14.4%; Score 263; DB 2; Length 707;

Best Local Similarity 25.9%; Pred. No. 1.2e-12;

Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

Db 24 COCEVETFGVDFPSU--TRVDSGSGPHMPVPIPLDPAHLDLSNRLEWVESVLAQP 81

33 CTCEIRPWFPRPRTIWEASTVDNDGLNFPARLADQIILLQNNIARIEHST--D 89

82 GYTTLAGLDLHNLTSISPTAFSRURYSLDLSHNGITLPAES-FTSSPLSDVNL 140

90 FPNVLTGLDLSQNNLSVTNINQKMSQLSVLEENKLEPEKLYGLSNLOELVNH 149

141 NQREVSVAFTHSQRALHVD-----LSHNLHRL----- 172

150 NLSALSPGAFVGLHNLRLHLSNRLQMINSKFPEALPNLGLDNPILRIKMFQ 209

173 -----VPHPTAGLPARTIQSLNLMNRLHVAVNL--RDLPRTYSL 212

210 PLTKRSLVAGINLVEPDDALVGL--ENLESISFDRNLKVPVALQKAVNLKFLDL 267

213 DGNPLAVIGPAGAGLGLTHLSLISQRLPELAPSGFRPLPGLQVLDLSGPKLNMAA 272

268 NKPIRIRRGDFSNMLHLELGINMPPELVISIDSLAVDNLPLRKIEATNPRLSYHP 327

273 EVFSGLSLQELDLSGNTLVPLPEALILHLPALQSVV--GDVRCRLVR---EGTYPR 327

328 NAFRLPKLESIMLNLSALVHGHTESLPNKEISHSNPIRCOCVIRMINMTNIR 367

328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Db 328 --RPGSSPKVPLHCVDTRE 344

388 FMEPDS-----LPCVDPPE 401

Best Local Similarity 29.8%; Pred. No. 5e-12;

Matches 89; Conservative 40; Mismatches 104; Indels 66; Gaps 9;

Db 6 LLLAVSGAQ-----TRPGCPGQCEVETFGVDFPSLTRYVDSGSGPHMPVPIPLDT 60

15 LLQVVAAGSSPGPDARPGCPHCHCL-----DGRMLRVCSDLGSELNLSVFT 68

61 AHDLSNRLEWVESVLAQPGYTTAGLDLSHNLTSISPTAFSRURYSLDLSHNGI 120

69 SYDLSNMNLSQPLASLT-----HRLCFEELRLAGNAL 102

121 TALAESEPT--SPSLDYNLSHNLREVSVAFTTHSGRALHYDLSHNLHRLVPHPTA 179

103 THIRKGAFTGLSHLKVLMQNLKRVPEALQNLNSLQSLRUDANH--ISVPPS--- 156

180 GLPAPTIQSLNLMNRLHVAVNLRLDPLRYLSLDGNPLAVIGPAGAGLGLTHLSL 239

157 -----CSGSLHS-----LRHLMDDNALTVPOAFRSLALQAMTLA-L 195

240 QRLPELAPSGRPLPGLQVLDLSGNPKLNMAAEVFGSLSLQELDLSGNTLVPLPEAL 298

196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

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Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

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Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

Db 196 NKIHIDYAFGNLSLVVHLHNN-RHSLGKKCFDGLHSLFTLDLNNNLDPEPTAI 253

A/Accession: A47507  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-560 <RES>  
 A/Cross-references: GB:L11238; NID:G388759; PID:AAA03069.1; PID:G388760  
 C/Comment: This platelet membrane protein is a substrate for thrombin.  
 C/Comment: The amino end of the intact protein is blocked.  
 C/Comment: This protein is absent in Bernard-Soulier syndrome.  
 C/Genetics:  
 A/Gene: GDB:GPS  
 A/Cross-references: GDB:230236; OMIM:173511  
 A/Map position: 5pter-5qter  
 C/Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
 C/Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot

Query Match 13.5%; Score 247; DB 2; Length 560;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-11;  
 Matches 112; Conservative 42; Mismatches 145; Indels 92; Gaps 14;

QY 7 LLLAVSAQOTR--PCPPGOC-----EVTFGFDSSTRVDCSG-- 48  
 DB 6 LLLAVGLRPAQPPCPACKCPVDAACSGGVDAISALGL--PTNLTHILLFGWGRG 63  
 QY 49 -----PHMPVP-----IPDTAHLDISNRL-----EWNES 76  
 DB 64 VLQSGSFGMTVLQRLMISDHSISAVAPGTFSDILKKT--LRLSRKTHLFGALIDKM 121  
 QY 77 VLAPGVTTLAAGLDSHNLTSISPTAFSRIRYESIDLSHNGLTALPASFTS----- 130  
 DB 122 VL-----LEQLFLDHNLALRGIDQNMFOKLVLNQLALNQMDLFPASLFTNLENTKL 174  
 QY 131 SPLDVNLISH-----NQLREVSAFTTHSGRALHVDLSHNLIRLV 173  
 DB 175 LDISGNLTHLPKGLLQAQKLERLLHSNRLVSLDGLANSGLATELQPHNRHSIA 234  
 QY 174 PHPTAGLPAFTTOSLNIAMNRLHAVPN--LRDLPLRYSLDGNPLAVIPGAFAGLG 230  
 DB 235 P---GAFDRPLNLSLTLSRHLAFPLPSALFHSNLTLLTLTFENPLAEIPGVLFGEWG 291  
 QY 231 LTHLSLALQRLPRLASPRELPGLOVLDSGNPKLWAGAEVFSGLSLQELDLSGTL 290  
 DB 292 LQELIMLRTO-LRLLPAAFRNLSRLRYLGVTLSPRLSALPQCAFQGLGQVLAHLSNG 350  
 QY 291 LVPLPEALLHLPALQSVGVQDVCRRIVR 321  
 DB 351 LTLALPDGLRGRLGRLQVSLRN-RLRALPR 380

## RESULT 7

NBH0A2  
 leucine-rich alpha-2-glycoprotein - human  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 05-Dec-1998  
 C/Accession: A03211  
 R/Takahashi, N.; Takahashi, Y.; Putnam, F.W.  
 A/Title: Periodicity of leucine and tandem repetition of a 24-amino acid segment in the  
 A/Reference number: A03211; MUID:8516241; PMID:3856868  
 A/Accession: A03211  
 A/Molecule type: protein  
 A/Residues: 1-312 <TAK>  
 C/Comment: The function of this plasma protein is not known.  
 C/Superfamily: leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein repe  
 C/Keywords: duplication; glycoprotein; plasma; tandem repeat  
 F/58-81/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F/82-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F/106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F/130-153/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F/154-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F/178-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F/202-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F/226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F/262-309/Domain: proteoglycan carboxyl-terminal homology <PCH>

F/2/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F/8-21,268-294/Disulfide bonds: #status experimental  
 F/44,151,234,290/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F/271/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 12.9%; Score 236.5; DB 1; Length 312;  
 Best Local Similarity 32.4%; Pred. No. 3e-11;  
 Matches 97; Conservative 34; Mismatches 109; Indels 59; Gaps 14;

QY 26 CEVETFGFDSFSLTRVDCSGGLPIMPEVPLDTHLHLSNRLEMVNESYLAQGYTT 85  
 DB 8 CCV-----FRSDHSGSISQ--PRAIEGYLADIVHLAVEFNNLTHLPANLQGA--SK 58  
 QY 86 LAGLDSHNLTSISPTAFSRIRYESIDLSHNGLTALPASBF-TSPSLDVNLHNOQL 144  
 DB 59 LQELHLSNGLSLSTPEFLRPVQRLVLDLTNNALTGPPGLFQASATLDTLVAKENOLE 118  
 QY 145 EVSVAFTTHSGRALHVDLSHNLIRLVPEPTRAGLPA--PTIOSLNIAMNRLHAVPN- 201  
 DB 119 VLFEVS--WLGKALGHLDLSGNRLKLP-----GLANFTLTLDDGEGQLETLPD 171  
 QY 202 -LR-DIPLRYSLDGNPLAVIPGAFAGLGLTHLSLALQRLPELASGFFRELPGLOVL 259  
 DB 172 LIRGPIQLERLHLEGNKQLQVLGKDL-----LPQ-----PDLRYL 206  
 QY 260 DISGNPKLWAGAEVFSGLSLQELDLSGTLNVLPLPEALLHLPALQSVSGO---DVR 315  
 DB 207 FLNNGN-KLARVAAGAFQGLRLDMDLDSNNSLASVBEGLM-----ASLQGPWDMK 256

## RESULT 8

JCS239  
 insulin-like growth factor acid-labile chain - baboon  
 C/Species: Papio sp. (baboon)  
 C/Date: 17-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-May-1997  
 C/Accession: JCS239  
 R/Delhanty, P.; Baxter, R.C.  
 A/Biochem. Biophys. Res. Commun. 227, 897-902, 1996  
 A/Title: The cloning and expression of the baboon acid-labile subunit of the insulin-l  
 A/Reference number: JCS239; MUID:97040714; PMID:886627  
 A/Contents: liver  
 A/Accession: JCS239  
 A/Molecule type: mRNA  
 A/Residues: 1-605 <DEL>  
 C/Comment: This factor is structurally related to proinsulin and have insulin-like met

Query Match 12.8%; Score 234.5; DB 2; Length 605;  
 Best Local Similarity 34.3%; Pred. No. 1.7e-10;  
 Matches 82; Conservative 21; Mismatches 95; Indels 41; Gaps 8;

QY 63 LDISNRLEMVNESYLAQGYTTLAGLDSHNLTSISPTAFSRIRYESIDLSHNGTLA 122  
 DB 271 LDISNRVAVGLLEDFP--PGLLGLVLRLSHNAIASLPRTBEDLHPELQGLGNRRIRQ 328  
 QY 123 LAESFTS-SPLSDVNLHNOQLREVSAFTTHSGRALHVDLSHNLIRLVPHPTRAGL 181  
 DB 329 LAERSEFGQLEVLTLHNOQLQEVKQAF-----L 359  
 QY 182 PAPTIOSLNIAMNRLHAVPN--LRDL-PLRYSLDGNPLAVIPGAFAGLGLTHLSIA- 237  
 DB 360 GLTNVAVMNLSCNCRLNPEQVFRGLGKLHSLHSGSCGRRPHTFAGLSGLRLFLKD 419  
 QY 238 -SLQRLPELASGFFRELPGLOVLDSGNPKLWAGAEVFSGLSLQELDLSGTLNVLPL 295  
 DB 420 NGIVGIEGOSLWGLAE--LLELDLTSN-QTLTHPQLFQGLGKLELYLLSHNRLAELP 474

## RESULT 9

AS8532  
 glial cell membrane glycoprotein LIG-1 precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 05-Nov-1999  
 C/Accession: AS8532





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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:18:07 ; Search time 39 Seconds

(Without alignments)  
2855.844 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1828  
Sequence: 1 MPWPLLLILAVSGAQTRPC.....KVPDLHCVDTRFSARSPITL 353

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mbc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	99.4	353	4	Q8WUA8
2	1815	99.3	353	4	Q9UUX6
3	1537	84.1	372	11	Q8CXB6
4	1235	67.6	242	4	Q9UG10
5	767	42.0	347	13	Q7ZUT1
6	311.5	17.0	713	4	Q8N182
7	263	14.4	707	11	Q9ESY6
8	261	14.3	707	11	Q97860
9	261	14.3	707	11	Q8CXB6
10	258	14.1	363	11	Q8C8A7
11	254	13.9	708	4	Q9H3W5
12	254	13.9	733	5	Q24250
13	254	13.9	737	5	Q9VU51
14	252.5	13.8	1360	5	Q9NDI1
15	251.5	13.8	542	5	Q9Y4G6
16	250	13.7	347	4	Q8Y4F5

17	250	13.7	718	13	Q73675	073675 xenopus lae
18	249.5	13.6	1065	4	Q94898	Q94898 homo sapien
19	249	13.6	1050	5	Q9EN18	Q9EN18 dirosophila
20	248	13.5	708	4	Q81Y06	Q81Y06 homo sapien
21	247.5	13.5	673	11	Q8BJT0	Q8BJT0 mus musculu
22	247.5	13.5	673	11	Q8R2G5	Q8R2G5 mus musculu
23	247	13.5	1392	5	Q9VAD1	Q9VAD1 dirosophila
24	245.5	13.4	1300	5	Q9NKD6	Q9NKD6 dirosophila
25	244.5	13.4	673	11	Q9CZT5	Q9CZT5 mus musculu
26	244.5	13.4	1029	6	Q866B2	Q866B2 bos taurus
27	243.5	13.3	1535	5	Q9VFP0	Q9VFP0 dirosophila
28	239.5	13.1	1022	6	Q8HXV0	Q8HXV0 bos taurus
29	238.5	13.0	342	11	Q91X11	Q91X11 mus musculu
30	238.5	13.0	811	4	Q75139	Q75139 homo sapien
31	238	13.0	927	4	Q9UGS3	Q9UGS3 homo sapien
32	238	13.0	927	4	Q8N537	Q8N537 homo sapien
33	235	12.9	453	4	Q86XY1	Q86XY1 homo sapien
34	235	12.9	1039	5	Q86B11	Q86B11 dirosophila
35	234.5	12.8	1514	5	Q9NBR9	Q9NBR9 dirosophila
36	234.5	12.8	1514	5	Q9VUN0	Q9VUN0 dirosophila
37	234	12.8	532	5	Q96671	Q96671 dirosophila
38	234	12.8	532	5	Q9VU53	Q9VU53 dirosophila
39	232	12.7	606	4	Q9B220	Q9B220 homo sapien
40	232	12.7	1104	10	Q7XUG6	Q7XUG6 oryza sativ
41	231.5	12.7	1512	13	Q9DE36	Q9DE36 brachydantio
42	231	12.6	606	11	Q8BZD4	Q8BZD4 mus musculu
43	231	12.6	606	11	Q8BLC0	Q8BLC0 mus musculu
44	230.5	12.6	928	4	Q95YD7	Q95YD7 homo sapien
45	230.5	12.6	1091	11	P70193	P70193 mus musculu
46	230	12.6	1094	4	Q9BYB8	Q9BYB8 homo sapien
47	229	12.5	391	11	Q9D3X0	Q9D3X0 mus musculu
48	228	12.5	579	11	Q8OX72	Q8OX72 mus musculu
49	228.5	12.5	363	4	Q9H5G9	Q9H5G9 homo sapien
50	228.5	12.5	1295	5	Q8T0X1	Q8T0X1 bombyx mori
51	228.5	12.5	1530	13	Q9QWZ3	Q9QWZ3 xenopus lae
52	228	12.5	1471	5	Q9VJQ0	Q9VJQ0 dirosophila
53	227.5	12.4	1459	5	Q8WRE4	Q8WRE4 anopheles g
54	226.5	12.4	1093	4	Q96JY1	Q96JY1 homo sapien
55	226	12.4	567	11	Q9QZU3	Q9QZU3 mus musculu
56	225.5	12.3	796	11	Q9WVCL	Q9WVCL rattus norv
57	225	12.3	1458	11	Q8CUG8	Q8CUG8 rattus norv
58	225	12.3	1530	11	Q9WUG5	Q9WUG5 rattus norv
59	225	12.3	1531	11	Q88279	Q88279 rattus norv
60	224	12.3	562	11	Q8H113	Q8H113 mus musculu
61	224	12.3	570	11	Q9PBB9	Q9PBB9 mus musculu
62	222	12.2	1474	11	Q8CTG9	Q8CTG9 rattus norv
63	222.5	12.2	605	4	Q8TAY0	Q8TAY0 homo sapien
64	222.5	12.2	1533	4	Q75094	Q75094 homo sapien
65	222	12.1	1030	6	Q865R8	Q865R8 sus scrofa
66	221.5	12.1	809	11	Q9DBY4	Q9DBY4 mus musculu
67	221.5	12.1	837	11	Q80TV0	Q80TV0 mus musculu
68	220	12.0	1521	11	Q9L1B9	Q9L1B9 mus musculu
69	220	12.0	1618	4	Q9U117	Q9U117 homo sapien
70	219.5	12.0	573	4	Q8EYH5	Q8EYH5 homo sapien
71	219.5	12.0	581	6	Q9BGP6	Q9BGP6 macaca fasc
72	219.5	12.0	1446	5	Q9V8Z0	Q9V8Z0 dirosophila
73	219	12.0	310	13	Q9BDZ8	Q9BDZ8 petromyzon
74	219	12.0	410	13	Q9DDZ7	Q9DDZ7 petromyzon
75	219	12.0	557	4	Q8N5V4	Q8N5V4 homo sapien
76	219	12.0	550	4	Q86SU4	Q86SU4 homo sapien
77	218.5	12.0	581	6	Q95K18	Q95K18 macaca fasc
78	218.5	12.0	603	11	Q70211	Q70211 rattus norv
79	218	11.9	466	11	Q8CJH0	Q8CJH0 rattus norv
80	218	11.9	611	11	Q7T062	Q7T062 mus musculu
81	218	11.9	1534	4	Q75093	Q75093 homo sapien
82	217	11.9	347	13	Q9DE00	Q9DE00 petromyzon
83	217	11.9	738	5	Q93373	Q93373 caenorhabdi
84	217	11.9	1531	11	Q9WYB5	Q9WYB5 mus musculu
85	217	11.9	1557	11	Q80TR4	Q80TR4 mus musculu
86	216	11.8	798	4	Q8WMZ2	Q8WMZ2 homo sapien
87	216	11.8	905	11	Q7TN18	Q7TN18 rattus norv
88	215.5	11.8	648	11	Q8V135	Q8V135 mus musculu
89	215.5	11.8	649	4	Q96A85	Q96A85 homo sapien

90	215.5	11.8	737	5	Q965M3	Q965M3 caenorhabdi	153	195.5	10.7	581	10	Q04143	Q04143 silene latf
91	215.5	11.8	881	5	Q965M2	Q965M2 caenorhabdi	154	195.5	10.7	633	11	Q08Y16	Q08Y16 mus musculu
92	215.5	11.8	1066	5	Q18902	Q18902 caenorhabdi	165	195.5	10.7	633	11	Q08R03	Q08R03 mus musculu
93	215.5	11.8	1447	5	Q16779	Q16779 caenorhabdi	166	195.5	10.7	669	11	Q08Y14	Q08Y14 mus musculu
94	215	11.8	514	11	Q08Z81	Q08Z81 mus musculu	167	195.5	10.7	675	11	Q08BMT4	Q08BMT4 mus musculu
95	215	11.8	582	11	Q08GJ7	Q08GJ7 mus musculu	168	195.5	10.7	721	11	Q08BUT7	Q08BUT7 mus musculu
96	215	11.8	1385	5	Q09VZ5	Q09VZ5 mus musculu	169	195.5	10.7	742	5	Q08BUD4	Q08BUD4 strongyloce
97	215	11.8	1389	5	Q24591	Q24591 drosophila	170	195	10.7	370	4	Q08N957	Q08N957 homo sapien
98	214.5	11.7	687	11	Q09J10	Q09J10 mus musculu	171	195	10.7	552	5	Q09V144	Q09V144 drosophila
99	214	11.7	544	13	Q08UV23	Q08UV23 spherooides	172	195	10.7	799	5	Q09V964	Q09V964 homo sapien
100	213.5	11.7	614	6	Q09N08	Q09N08 macaca fasc	173	194.5	10.6	1024	2	Q0841E6	Q0841E6 raiistonia s
101	213.5	11.7	652	11	Q099PH1	Q099PH1 mus musculu	174	194.5	10.6	1024	2	Q0841E6	Q0841E6 raiistonia s
102	213.5	11.7	653	4	Q09BMT1	Q09BMT1 homo sapien	175	194	10.6	332	13	Q08QFN6	Q08QFN6 elaphe quad
103	213.5	11.7	923	4	Q08VU0	Q08VU0 homo sapien	176	194	10.6	515	11	Q08C911	Q08C911 mus musculu
104	213.5	11.7	923	4	Q08VU0	Q08VU0 homo sapien	177	194	10.6	515	11	Q08C911	Q08C911 mus musculu
105	212.5	11.6	716	11	Q061809	Q061809 mus musculu	178	194	10.6	515	11	Q08C911	Q08C911 mus musculu
106	212.5	11.6	613	4	Q72517	Q72517 homo sapien	179	194	10.6	719	4	Q06N16	Q06N16 homo sapien
107	212	11.6	1052	4	Q09V4C4	Q09V4C4 mus musculu	180	194	10.6	719	4	Q06N16	Q06N16 homo sapien
108	212	11.6	1523	11	Q09WVB4	Q09WVB4 mus musculu	181	194	10.6	719	11	Q08BXA0	Q08BXA0 mus musculu
109	211.5	11.6	359	13	Q09DE03	Q09DE03 oreochromis	182	194	10.6	746	11	Q08ZL0	Q08ZL0 mus musculu
110	211.5	11.6	606	11	Q77T38	Q77T38 mus musculu	183	194	10.6	940	5	Q08T753	Q08T753 drosophila
111	211.5	11.6	614	11	Q09D10	Q09D10 mus musculu	184	194	10.6	1051	5	Q24007	Q24007 drosophila
112	211	11.5	602	11	Q08S83	Q08S83 mus musculu	185	194	10.6	1076	5	Q08M174	Q08M174 drosophila
113	211	11.5	636	11	Q08K3C4	Q08K3C4 mus musculu	186	193.5	10.5	1051	5	Q095PA9	Q095PA9 drosophila
114	211	11.5	636	11	Q08K3C4	Q08K3C4 mus musculu	187	193	10.5	1051	5	Q095PA9	Q095PA9 drosophila
115	211	11.5	716	4	Q08YV5	Q08YV5 homo sapien	188	192.5	10.5	370	11	Q08BXC3	Q08BXC3 mus musculu
116	211	11.5	730	4	Q09P231	Q09P231 homo sapien	189	192	10.5	399	11	Q08B45	Q08B45 mus musculu
117	211	11.5	1012	5	Q09Y176	Q09Y176 asterina pe	190	192	10.5	577	13	Q08AY14	Q08AY14 xenopus lae
118	211	11.5	1280	5	Q095Y17	Q095Y17 asterina pe	191	192	10.5	1778	16	Q08Y32	Q08Y32 listeria mo
119	210.5	11.5	518	11	Q08OXG9	Q08OXG9 mus musculu	192	191.5	10.5	311	16	Q08F116	Q08F116 mus musculu
120	210.5	11.5	591	11	Q08Z80	Q08Z80 mus musculu	193	191.5	10.5	565	11	Q08C030	Q08C030 mus musculu
121	210.5	11.5	1523	11	Q08Z80	Q08Z80 mus musculu	194	191.5	10.5	878	11	Q08KX59	Q08KX59 mus musculu
122	210	11.5	582	11	Q08Z80	Q08Z80 mus musculu	195	191	10.4	402	4	Q03300	Q03300 homo sapien
123	210	11.5	739	11	Q08KX5	Q08KX5 mus musculu	196	191	10.4	516	4	Q03300	Q03300 homo sapien
124	210	11.5	836	10	Q09SC14	Q09SC14 arabidopsis	197	190.5	10.4	518	13	Q07SYC0	Q07SYC0 drosophila
125	209.5	11.5	373	13	Q0803T1	Q0803T1 brachydando	198	190.5	10.4	534	5	Q08Y79	Q08Y79 drosophila
126	208	11.4	388	13	Q09D29	Q09D29 petromyzon	199	190.5	10.4	677	6	Q08Z56	Q08Z56 mus musculu
127	208	11.4	602	5	Q093377	Q093377 caenorhabdi	200	190.5	10.4	947	10	Q08RUT5	Q08RUT5 oryza sativ
128	207.5	11.4	548	5	Q09VU1	Q09VU1 drosophila	201	189.5	10.4	628	4	Q09B10	Q09B10 homo sapien
129	207.5	11.4	640	4	Q09HC12	Q09HC12 homo sapien	202	189	10.3	332	13	Q08CPN7	Q08CPN7 mus musculu
130	207.5	11.4	640	11	Q08C031	Q08C031 mus musculu	203	189	10.3	785	4	Q09P263	Q09P263 homo sapien
131	207.5	11.4	640	11	Q08C031	Q08C031 mus musculu	204	189	10.3	1036	10	Q09FN37	Q09FN37 arabidopsis
132	207.5	11.3	273	4	Q09NU04	Q09NU04 homo sapien	205	188.5	10.3	499	10	Q08VY9	Q08VY9 arabidopsis
133	206.5	11.3	615	5	Q09VZ84	Q09VZ84 drosophila	206	188	10.3	329	5	Q09VY8	Q09VY8 drosophila
134	206	11.3	622	4	Q07Z207	Q07Z207 homo sapien	207	188	10.3	1179	6	Q09B86	Q09B86 macaca fasc
135	205	11.2	491	5	Q09VX6	Q09VX6 drosophila	208	187.5	10.3	522	4	Q09DUN1	Q09DUN1 homo sapien
136	205	11.2	1079	6	Q085B39	Q085B39 canis famli	209	187.5	10.3	522	4	Q086D6	Q086D6 homo sapien
137	204.5	11.2	601	4	Q096CX1	Q096CX1 homo sapien	210	187.5	10.3	626	11	Q08LY3	Q08LY3 mus musculu
138	204	11.2	582	11	Q08BYL0	Q08BYL0 mus musculu	211	187.5	10.3	649	11	Q08BGT1	Q08BGT1 mus musculu
139	204	11.2	1515	13	Q09DE37	Q09DE37 brachydando	212	187.5	10.3	893	4	Q096C25	Q096C25 homo sapien
140	204	11.2	1529	13	Q07X12	Q07X12 xenopus lae	213	187.5	10.3	910	4	Q09H75	Q09H75 homo sapien
141	203.5	11.1	1031	6	Q08H52	Q08H52 felis silve	214	187.5	10.3	1247	5	Q09B86	Q09B86 drosophila
142	203	11.1	524	11	Q08R378	Q08R378 mus musculu	215	187.5	10.3	1756	5	Q09B86	Q09B86 drosophila
143	203	11.1	524	5	Q03580	Q03580 caenorhabdi	216	187.5	10.3	1756	5	Q09B86	Q09B86 drosophila
144	202.5	11.1	575	5	Q03580	Q03580 caenorhabdi	217	187.5	10.3	1850	5	Q09B86	Q09B86 drosophila
145	202	11.1	581	4	Q09BTR7	Q09BTR7 homo sapien	218	187	10.2	554	5	Q09VDD5	Q09VDD5 drosophila
146	202	11.1	602	4	Q09H9A6	Q09H9A6 homo sapien	219	186.5	10.2	770	10	Q09VY8	Q09VY8 drosophila
147	201.5	11.0	526	10	Q07XJ53	Q07XJ53 arabidopsis	220	186.5	10.2	420	4	Q08DUN3	Q08DUN3 homo sapien
148	201.5	11.0	680	5	Q093374	Q093374 caenorhabdi	221	186	10.2	471	10	Q09LVR8	Q09LVR8 arabidopsis
149	201.5	11.0	1259	11	Q08BAX7	Q08BAX7 mus musculu	222	184.5	10.1	287	5	Q092B9	Q092B9 ratu
150	201	11.0	951	5	P090920	P090920 caenorhabdi	223	184	10.1	420	11	Q08OWD1	Q08OWD1 ratu
151	200.5	11.0	470	5	Q09V354	Q09V354 drosophila	224	184	10.1	633	16	Q08F3F6	Q08F3F6 leprospira
152	200	10.9	1077	5	Q09NUG7	Q09NUG7 drosophila	225	184	10.1	521	11	Q08BHA1	Q08BHA1 mus musculu
153	199	10.9	1119	16	Q08Z0H2	Q08Z0H2 anabaena sp	226	183.5	10.0	597	5	Q09V09	Q09V09 drosophila
154	198.5	10.9	741	5	Q09VJ49	Q09VJ49 drosophila	227	183.5	10.0	785	10	Q09LVN2	Q09LVN2 arabidopsis
155	198	10.8	364	11	Q08B551	Q08B551 mus musculu	228	183	10.0	1275	16	Q09VY40	Q09VY40 streptococ
156	198	10.8	953	5	Q09V701	Q09V701 drosophila	229	183	10.0	1275	16	Q08NZK6	Q08NZK6 streptococ
157	198	10.8	1346	5	Q09V477	Q09V477 drosophila	230	183	10.0	1275	16	Q08K600	Q08K600 streptococ
158	197.5	10.8	894	5	Q08JUD6	Q08JUD6 strongyloce	231	183	10.0	1277	16	Q0879K2	Q0879K2 streptococ
159	197.5	10.8	1152	5	Q08RME5	Q08RME5 anopheles g	232	183	10.0	1277	16	Q0879K2	Q0879K2 streptococ
160	196.5	10.7	1221	5	Q09BIM9	Q09BIM9 caenorhabdi	233	183	10.0	423	5	Q09V025	Q09V025 drosophila
161	196.5	10.7	1221	5	Q09NS23	Q09NS23 caenorhabdi	234	182.5	10.0	423	5	Q08F751	Q08F751 leprospira
162	195.5	10.7	372	13	Q07T2W3	Q07T2W3 brachydando	235	182.5	10.0	440	11	Q07TQ25	Q07TQ25 ratu

236	182.5	10.0	440	11	Q7TMM3	Q7Tm3 ratius novr	309	171.5	9.4	537	5	Q9VE49	Q9ve49 drosophila
237	182.5	10.0	522	11	Q8K377	Q8K377 mus musculu	310	171.5	9.4	550	10	Q9AX18	Q9ax18 oryza sativ
238	182.5	10.0	535	10	Q8RX50	Q8RX50 brasiica ni	311	171.5	9.4	586	5	Q21164	Q21164 caenorhabdi
239	182.5	10.0	1356	5	Q8WR82	Q8WR82 anopheles g	312	171.5	9.4	626	4	Q8N1P3	Q8n1f3 homo sapien
240	182	10.0	492	11	Q99KT6	Q99KT6 mus musculu	313	171.5	9.4	626	4	Q8NG39	Q8ng39 homo sapien
241	181.5	9.9	584	10	Q49751	Q49751 arabidopsis	314	171.5	9.4	682	5	Q9VZ74	Q9vz74 drosophila
242	181.5	9.9	584	10	Q81722	Q81722 arabidopsis	315	171.5	9.4	1002	10	Q9ARQ7	Q9arq7 oryza sativ
243	181.5	9.9	915	11	Q9ERV7	Q9ERV7 mus musculu	316	171.5	9.4	1101	10	Q9FMT8	Q9fm8 oryza sativ
244	181.5	9.9	1028	6	Q85ER7	Q85ER7 sus scrofa	317	171.5	9.4	1101	10	Q7XDJ5	Q7xdj5 oryza sativ
245	181.5	9.9	1135	10	Q7X511	Q7X511 oryza sativ	318	171	9.4	954	5	Q9VJ07	Q9vj07 drosophila
246	181	9.9	853	11	Q8CB40	Q8CB40 mus musculu	319	171	9.4	2964	5	Q81VW7	Q81vw7 dictyosteli
247	181	9.9	1076	5	Q8MQU7	Q8mqU7 aedes aegy	320	170.5	9.3	584	10	Q49750	Q49750 arabidopsis
248	180.5	9.9	224	13	Q9DE01	Q9de01 brachydantio	321	170.5	9.3	601	13	Q7SXM3	Q7sxm3 Q9v50 brachydantio
249	180.5	9.9	343	5	Q9WZ17	Q9WZ17 drosophila	322	170.5	9.3	892	5	P91644	P91644 drosophila
250	180.5	9.9	426	16	Q8RF13	Q8RF13 leptospira	323	170.5	9.3	894	5	Q9YKG1	Q9ykg1 drosophila
251	180.5	9.9	977	10	Q7XN51	Q7XN51 oryza sativ	324	170.5	9.3	1016	10	Q91RPT	Q91rpt arabidopsis
252	180	9.8	288	11	Q8BR15	Q8BR15 mus musculu	325	170.5	9.3	1143	10	Q8SUD9	Q8sud9 arabidopsis
253	180	9.8	497	10	Q7XKC0	Q7XKC0 oryza sativ	326	170	9.3	376	4	Q81V47	Q81v47 homo sapien
254	180	9.8	613	10	Q940E8	Q940E8 zea mays (m	327	170	9.3	512	11	Q9CQ76	Q9cq76 mus musculu
255	179.5	9.8	530	11	Q80WQ1	Q80WQ1 mus musculu	328	170	9.3	583	11	Q8BM77	Q8bm77 mus musculu
256	179.5	9.8	1102	16	Q8KC98	Q8KC98 chlorobium	329	170	9.3	631	17	Q8TN14	Q8tn14 methanosarc
257	179	9.8	428	4	Q14498	Q14498 homo sapien	330	169.5	9.3	408	16	Q8F212	Q8f212 leptospira
258	179	9.8	463	11	Q8C1V9	Q8C1V9 mus musculu	331	169.5	9.3	623	5	Q9SS21	Q9ss21 drosophila
259	179	9.8	496	10	Q8GWY1	Q8GWY1 arabidopsis	332	169.5	9.3	893	10	Q9SWE6	Q9swe6 hordeum vul
260	179	9.8	933	5	Q9BDJ5	Q9BDJ5 strongyloce	333	169.5	9.3	1012	10	Q7XPT3	Q7xpt3 oryza sativ
261	179	9.8	1172	10	Q9FMM3	Q9FMM3 oryza sativ	334	169.5	9.3	1130	10	Q8SB68	Q8sb68 oryza sativ
262	179	9.8	1175	10	Q7XDK0	Q7XDK0 oryza sativ	335	169.5	9.3	1130	10	Q7XGP4	Q7xgp4 oryza sativ
263	179	9.8	1410	5	Q20204	Q20204 caenorhabdi	336	169	9.2	437	13	Q9DE05	Q9deg5 gallus galli
264	178.5	9.8	1257	5	Q9VXR8	Q9VXR8 drosophila	337	169	9.2	893	10	Q8LKR3	Q8lkr3 glycine max
265	178	9.7	734	11	Q35330	Q35330 mus musculu	338	169	9.2	964	10	Q8VY77	Q8vy77 arabidopsis
266	178	9.7	966	10	Q9LNX3	Q9LNX3 arabidopsis	339	169	9.2	964	10	Q9L1Y3	Q9l1y3 arabidopsis
267	178	9.7	1007	5	Q8MCU9	Q8mcU9 aedes aegy	340	168.5	9.2	1030	10	Q8H037	Q8h037 oryza sativ
268	177.5	9.7	537	10	Q9C769	Q9C769 arabidopsis	341	168	9.2	395	10	Q9ZT98	Q9zt98 arabidopsis
269	177.5	9.7	627	4	Q8NC95	Q8NC95 homo sapien	342	168	9.2	510	6	Q9BGY6	Q9bgy6 macaca fasc
270	177	9.7	428	16	Q8F3F8	Q8F3F8 leptospira	343	168	9.2	753	4	Q9NIR6	Q9nir6 homo sapien
271	177	9.7	562	10	Q9MTW9	Q9MTW9 arabidopsis	344	167.5	9.2	510	5	Q9NIR8	Q9nir8 dictyosteli
272	177	9.7	692	4	Q86Y13	Q86Y13 homo sapien	345	167	9.1	423	4	Q8ND46	Q8nd46 homo sapien
273	177	9.7	727	6	Q8HXC8	Q8HXC8 macaca fasc	346	167	9.1	483	5	Q9SSP1	Q9ssp1 drosophila
274	176.5	9.7	353	13	Q7SY88	Q7SY88 xenopus lae	347	167	9.1	533	5	Q9VHV3	Q9vhw3 drosophila
275	176.5	9.7	369	11	Q7TWM3	Q7TWM3 mus musculu	348	167	9.1	603	5	Q22075	Q22075 caenorhabdi
276	176.5	9.7	594	10	Q91UQ2	Q91UQ2 arabidopsis	349	167	9.1	664	13	Q7ZT81	Q7zt81 oncorhynch
277	176.5	9.7	1112	10	Q41397	Q41397 lycopersico	350	167	9.1	693	4	Q7Z3D0	Q7z3d0 homo sapien
278	176.5	9.7	1112	10	Q41398	Q41398 lycopersico	351	167	9.1	855	10	Q9ZS83	Q9zs83 lycopersico
279	176	9.6	653	5	Q02329	Q02329 caenorhabdi	352	167	9.1	892	10	Q84WPI	Q84wpi arabidopsis
280	176	9.6	864	10	Q8LPG4	Q8LPG4 arabidopsis	353	167	9.1	893	10	Q9LNX8	Q9lnx8 arabidopsis
281	176	9.6	864	10	Q9T033	Q9T033 arabidopsis	354	167	9.1	1013	10	Q8LQ10	Q8lq10 oryza sativ
282	176	9.6	1048	10	Q8VYQ5	Q8VYQ5 arabidopsis	355	167	9.1	1095	13	Q90XG4	Q90xg4 gallus galli
283	176	9.6	1200	5	Q86OS7	Q86OS7 arabidopsis	356	166.5	9.1	213	6	Q865R9	Q865r9 sus scrofa
284	176	9.6	1271	11	Q8VT44	Q8VT44 mus musculu	357	166.5	9.1	606	10	Q8H609	Q8h609 oryza sativ
285	176	9.6	1271	11	Q931Z8	Q931Z8 mus musculu	358	166.5	9.1	967	10	Q9LZV7	Q9lzv7 arabidopsis
286	175.5	9.6	452	16	Q8F118	Q8F118 leptospira	359	166.5	9.1	977	10	Q8GWNO	Q8gwno oryza sativ
287	175.5	9.6	506	10	Q9FPJ3	Q9FPJ3 arabidopsis	360	166.5	9.1	1008	10	Q8L1Z6	Q8l1z6 glycine max
288	175	9.6	721	4	Q9NUY1	Q9NUY1 homo sapien	361	166.5	9.1	1274	10	Q8L1S5	Q8l1s5 oryza sativ
289	175	9.6	865	10	Q50022	Q50022 lycopersico	362	166	9.1	865	10	Q9ZS79	Q9zs79 lycopersico
290	175	9.6	1369	4	Q60346	Q60346 homo sapien	363	166	9.1	1012	10	Q9LXZ4	Q9lxz4 glycine max
291	175	9.6	1696	11	Q9WNR8	Q9WNR8 ratus norv	364	165.5	9.1	441	4	Q8N6V2	Q8n6v2 homo sapien
292	175	9.6	370	13	Q9DNR4	Q9DNR4 orochromis	365	165.5	9.1	647	5	Q86NWS	Q86nws drosophila
293	174	9.5	378	11	Q8CAZ9	Q8CAZ9 mus musculu	366	165.5	9.1	650	5	Q9V3X1	Q9v3x1 drosophila
294	174	9.5	462	10	Q9SUH6	Q9SUH6 arabidopsis	367	165.5	9.1	825	5	Q96M63	Q96m63 homo sapien
295	174	9.5	1205	5	Q86QTO	Q86QTO drosophila	368	165	9.0	215	11	Q91VH8	Q91vh8 mus musculu
296	173.5	9.5	441	4	Q86UN2	Q86UN2 homo sapien	369	165	9.0	607	10	Q9LS89	Q9ls89 arabidopsis
297	173.5	9.5	646	11	Q8BJH4	Q8BJH4 mus musculu	370	165	9.0	783	13	Q90XG2	Q90xg2 gallus galli
298	173.5	9.5	840	11	Q8C110	Q8C110 mus musculu	371	165	9.0	789	6	Q9BE71	Q9be71 macaca fasc
299	173	9.5	404	11	Q7TP21	Q7TP21 mus musculu	372	165	9.0	832	4	Q9UTM4	Q9utm4 homo sapien
300	173	9.5	494	5	Q9VEK6	Q9VEK6 drosophila	373	165	9.0	950	13	Q90Z44	Q90z44 gallus galli
301	173	9.5	527	5	Q86P35	Q86P35 drosophila	374	165	9.0	1143	10	Q9ZP89	Q9zp89 arabidopsis
302	173	9.5	641	5	Q8MQMO	Q8mqmO drosophila	375	165	9.0	1174	10	Q7XTU4	Q7xtu4 oryza sativ
303	173	9.5	915	5	Q9WZ67	Q9WZ67 drosophila	376	165	9.0	1535	5	Q23991	Q23991 drosophila
304	173	9.5	1318	11	Q8CH84	Q8CH84 mus musculu	377	164.5	9.0	425	10	Q9FK66	Q9fk66 arabidopsis
305	172.5	9.4	304	11	Q9SZQ9	Q9SZQ9 arabidopsis	378	164.5	9.0	426	11	Q8BOA4	Q8bqa4 mus musculu
306	172	9.4	406	10	Q8BNJ3	Q8bnj3 mus musculu	379	164.5	9.0	469	5	Q9W128	Q9w128 drosophila
307	172	9.4	1034	10	Q7XKS4	Q7XKS4 oryza sativ	380	164.5	9.0	549	10	Q9SVW8	Q9svw8 arabidopsis
308	171.5	9.4	443	11	Q9CXD9	Q9CXD9 mus musculu	381	164.5	9.0	656	5	Q19312	Q19312 caenorhabdi

382	164.5	9.0	853	11	Q8GCR9	Q8GCR9 mus musculus	455	157	8.6	626	11	Q921U9	Q921U9 mus musculus
383	164.5	9.0	966	10	Q9FG25	Q9FG25 arabidopsis	456	157	8.6	732	5	Q8MRP3	Q8MRP3 drosophila
384	164.5	9.0	966	10	Q8GY29	Q8GY29 arabidopsis	457	157	8.6	862	10	Q50020	Q50020 lycopersico
385	164.5	9.0	1178	10	Q942T3	Q942T3 oryza sativ	458	157	8.6	938	10	Q91VB3	Q91VB3 arabidopsis
386	164	9.0	420	4	Q13641	Q13641 homo sapien	459	157	8.6	1025	10	Q40640	Q40640 oryza sativ
387	164	9.0	737	10	Q85700	Q85700 oryza sativ	460	157	8.6	1110	10	Q94LNL2	Q94LNL2 oryza sativ
388	164	9.0	740	10	Q49325	Q49325 arabidopsis	461	156.5	8.6	457	5	Q960D1	Q960D1 drosophila
389	164	9.0	950	4	Q95804	Q95804 homo sapien	462	156.5	8.6	646	16	Q8PDD3	Q8PDD3 xanthomonas
390	164	9.0	1159	10	Q8H4D0	Q8H4D0 oryza sativ	463	156.5	8.6	863	10	Q40235	Q40235 lycopersico
391	163.5	8.9	426	11	Q90YD9	Q90YD9 ratius norv	464	156.5	8.6	1053	10	Q94G61	Q94G61 lycopersico
392	163.5	8.9	620	11	Q8XZN9	Q8XZN9 talstonia s	465	156.5	8.6	1527	5	Q9VZ24	Q9VZ24 drosophila
393	163.5	8.9	833	11	Q80T99	Q80T99 mus musculus	466	156	8.5	399	5	Q8STX6	Q8STX6 encephalito
394	163	8.9	635	5	Q93539	Q93539 caenorhabdi	467	156	8.5	837	6	Q8SPE8	Q8SPE8 gorilla gor
395	163	8.9	655	5	Q50028	Q50028 lycopersico	468	156	8.5	853	10	Q8RWC6	Q8RWC6 arabidopsis
396	163	8.9	1035	11	Q92166	Q92166 mus musculus	469	156	8.5	1344	10	Q9SKW9	Q9SKW9 oryza sativ
397	163	8.9	1135	10	Q8W0A8	Q8W0A8 oryza sativ	470	155.5	8.5	180	11	Q8BPJ0	Q8BPJ0 mus musculus
398	163	8.9	2271	3	Q9C443	Q9C443 cryplococcu	471	155.5	8.5	371	10	Q9A1N5	Q9A1N5 oryza sativ
399	162.5	8.9	426	11	Q920L0	Q920L0 mus musculus	472	155.5	8.5	371	10	Q7XRC9	Q7XRC9 oryza sativ
400	162.5	8.9	581	11	Q9D5O5	Q9D5O5 mus sapien	473	155.5	8.5	505	10	Q7XK44	Q7XK44 mus musculus
401	162.5	8.9	674	4	Q8WVA2	Q8WVA2 homo sapien	474	155.5	8.5	788	11	Q9CYK3	Q9CYK3 oryza sativ
402	162.5	8.9	1600	10	Q9SM84	Q9SM84 oryza sativ	475	155.5	8.5	988	10	Q8L0I9	Q8L0I9 oryza sativ
403	162	8.9	581	2	Q9AN90	Q9AN90 bradyrhizob	476	155.5	8.5	1015	10	Q949G9	Q949G9 malus flori
404	162	8.9	585	16	Q89TLL5	Q89TLL5 bradyrhizob	477	155.5	8.5	1053	10	Q94G62	Q94G62 lycopersico
405	162	8.9	636	6	Q8SQH3	Q8SQH3 canis famli	478	155	8.5	543	10	Q8S7M7	Q8S7M7 oryza sativ
406	162	8.9	855	10	Q50023	Q50023 lycopersico	479	155	8.5	590	11	Q8P2F4	Q8P2F4 mus musculus
407	162	8.9	966	10	Q94JU3	Q94JU3 oryza sativ	480	155	8.5	685	16	Q8F1V0	Q8F1V0 leptospira
408	162	8.9	1010	10	Q8H3W8	Q8H3W8 oryza sativ	481	155	8.5	753	10	Q8SB69	Q8SB69 oryza sativ
409	162	8.9	1100	5	Q24622	Q24622 drosophila	482	155	8.5	1155	10	Q8S659	Q8S659 oryza sativ
410	162	8.9	1278	10	Q9AV65	Q9AV65 oryza sativ	483	155	8.5	1155	10	Q7XG55	Q7XG55 oryza sativ
411	162	8.9	1278	10	Q7XDK3	Q7XDK3 oryza sativ	484	155	8.5	1343	10	Q7XWN3	Q7XWN3 oryza sativ
412	162	8.9	1420	10	Q9XE13	Q9XE13 oryza sativ	485	155	8.5	2155	3	Q9HEP4	Q9HEP4 blumeria gr
413	161.5	8.8	243	11	Q8CEB3	Q8CEB3 mus musculi	486	154.5	8.5	394	10	Q8WEJ9	Q8WEJ9 oryza sativ
414	161.5	8.8	417	6	Q8H251	Q8H251 canis famli	487	154.5	8.5	394	10	Q7XK49	Q7XK49 oryza sativ
415	161.5	8.8	866	10	Q50021	Q50021 lycopersico	488	154.5	8.5	535	10	Q9AV64	Q9AV64 oryza sativ
416	161.5	8.8	945	13	Q801P9	Q801P9 carassius a	489	154.5	8.5	535	10	Q7XDK2	Q7XDK2 oryza sativ
417	161	8.8	589	10	Q9FHL8	Q9FHL8 arabidopsis	490	154.5	8.5	976	10	Q42371	Q42371 arabidopsis
418	160.5	8.8	1181	13	Q7Z235	Q7Z235 brachydantio	491	154.5	8.5	1630	4	Q8MWV8	Q8MWV8 homo sapien
419	160	8.8	440	4	Q9HSY7	Q9HSY7 homo sapien	492	154.5	8.5	1630	4	Q14160	Q14160 homo sapien
420	160	8.8	528	5	Q01764	Q01764 caenorhabdi	493	154.5	8.5	1665	11	Q8V1I1	Q8V1I1 mus musculus
421	160	8.8	1134	10	Q65510	Q65510 arabidopsis	494	154.5	8.5	1694	11	Q80U72	Q80U72 mus musculus
422	160	8.8	1866	4	Q86W13	Q86W13 homo sapien	495	154.5	8.5	2309	3	Q8WZV3	Q8WZV3 neurospora
423	159.5	8.7	1494	10	Q9AXA4	Q9AXA4 oryza sativ	496	154	8.4	471	5	Q9VBR3	Q9VBR3 drosophila
424	159.5	8.7	558	5	Q8MP65	Q8MP65 caenorhabdi	497	154	8.4	720	10	Q9SPE9	Q9SPE9 arabidopsis
425	159.5	8.7	559	5	Q22875	Q22875 caenorhabdi	498	154	8.4	720	10	Q80809	Q80809 arabidopsis
426	159.5	8.7	1124	5	Q8WQ08	Q8WQ08 aedes aegypt	499	154	8.4	720	10	Q9SPE8	Q9SPE8 arabidopsis
427	159.5	8.7	1140	10	Q9LR04	Q9LR04 arabidopsis	500	154	8.4	890	10	Q48849	Q48849 arabidopsis
428	159	8.7	493	11	Q80ZD7	Q80ZD7 ratius norv							
429	159	8.7	507	5	Q9N3F2	Q9N3F2 caenorhabdi							
430	159	8.7	720	10	Q50027	Q50027 lycopersico							
431	159	8.7	810	5	Q8T3J2	Q8T3J2 drosophila							
432	159	8.7	811	5	Q9VK54	Q9VK54 drosophila							
433	159	8.7	820	11	Q9DS57	Q9DS57 mus musculi							
434	159	8.7	880	5	P91643	P91643 drosophila							
435	159	8.7	999	10	Q82432	Q82432 malus domes							
436	158.5	8.7	478	10	Q9FW48	Q9FW48 arabidopsis							
437	158.5	8.7	480	10	Q48705	Q48705 arabidopsis							
438	158.5	8.7	493	4	Q81W71	Q81W71 homo sapien							
439	158.5	8.7	493	4	Q86WK6	Q86WK6 homo sapien							
440	158.5	8.7	792	13	Q90243	Q90243 gallus galli							
441	158.5	8.7	809	10	Q9Z0H2	Q9Z0H2 arabidopsis							
442	158.5	8.7	839	6	Q8M102	Q8M102 cryctolagus							
443	158.5	8.7	843	13	Q7ZRG5	Q7ZRG5 gallus galli							
444	158.5	8.7	862	10	Q50026	Q50026 lycopersico							
445	158.5	8.7	938	10	Q84XU7	Q84XU7 elaeis guin							
446	158.5	8.7	994	10	Q85B35	Q85B35 oryza sativ							
447	158	8.6	768	10	Q9Z581	Q9Z581 lycopersico							
448	157.5	8.6	325	4	Q8NA57	Q8NA57 homo sapien							
449	157.5	8.6	464	10	Q8WAQ3	Q8WAQ3 arabidopsis							
450	157.5	8.6	828	6	Q8SPE9	Q8SPE9 pongo pygma							
451	157	8.6	332	10	Q8GT95	Q8GT95 oryza sativ							
452	157	8.6	492	11	Q80ZD8	Q80ZD8 mus musculi							
453	157	8.6	540	5	Q9NKR4	Q9NKR4 drosophila							
454	157	8.6	550	5	Q9V0N8	Q9V0N8 drosophila							

## ALIGNMENTS

RESULT 1

ID Q8WU8 PRELIMINARY; PRT; 353 AA.

AC Q8WU8; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 24, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RL Struhsberg R.;

RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Kalline N., Chen X., Rolfs A., Halleck A., Hines J., Eisenstein S.,

RA Koudinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,

RA Phelan M., Farmer A.;

RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor

RT vector." ;

DR EMBL; BC020975; AA020975.1 ;

DR EMBL; BT007440; AAP36108.1 ;

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000372; LRR\_Nterm.

DR InterPro; IPR003591; LRR\_Cyp.

DR Pfam; PF00560; LRR\_5.

DR PRINTS; PR00019; LEURICHRPT.

DR SMART; SM00013; LRRNT; 1.

DR SMART; SM00369; LRR\_Typ; 1.

KM Hypothetical protein.

SQ SEQUENCE 353 AA; 37807 MW; 80F073221B8A38A5 CRC64;

Query Match 99.4%; Score 1817; DB 4; Length 353;

Best Local Similarity 99.4%; Pred. No. 5.2e-132;

Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 MPWLLILLAVSAGQTRPCPGCCQCEVETFGLEFDSFLTRVDCSGGLGPHIMPVPIPLDT 60

DB 1 MPWLLILLAVSAGQTRPCPGCCQCEVETFGLEFDSFLTRVDCSGGLGPHIMPVPIPLDT 60

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 121 TALPAESFTSSPLSDVNSHNLREVSAPFTTHSQGRALHVDLSHNLHRLVPHPTAG 180

DB 121 TALPAESFTSSPLSDVNSHNLREVSAPFTTHSQGRALHVDLSHNLHRLVPHPTAG 180

DB 181 LPAPTIQSINLAWNRLHAPNRLDPLRYSLDGNPLAVIGGAFAGIGLTHLSLASIQ 240

DB 181 LPAPTIQSINLAWNRLHAPNRLDPLRYSLDGNPLAVIGGAFAGIGLTHLSLASIQ 240

DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSLOELDLSGTLVLPPEALL 300

DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSLOELDLSGTLVLPPEALL 300

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

SQ SEQUENCE 353 AA; 37830 MW; CSEEA79B06FEFF8 CRC64;

Query Match 99.3%; Score 1815; DB 4; Length 353;

Best Local Similarity 99.4%; Pred. No. 7.4e-132;

Matches 351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 MPWLLILLAVSAGQTRPCPGCCQCEVETFGLEFDSFLTRVDCSGGLGPHIMPVPIPLDT 60

DB 1 MPWLLILLAVSAGQTRPCPGCCQCEVETFGLEFDSFLTRVDCSGGLGPHIMPVPIPLDT 60

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 61 AHLDSSNRLMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRRLYLSLDSHNGL 120

DB 121 TALPAESFTSSPLSDVNSHNLREVSAPFTTHSQGRALHVDLSHNLHRLVPHPTAG 180

DB 121 TALPAESFTSSPLSDVNSHNLREVSAPFTTHSQGRALHVDLSHNLHRLVPHPTAG 180

DB 181 LPAPTIQSINLAWNRLHAPNRLDPLRYSLDGNPLAVIGGAFAGIGLTHLSLASIQ 240

DB 181 LPAPTIQSINLAWNRLHAPNRLDPLRYSLDGNPLAVIGGAFAGIGLTHLSLASIQ 240

DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSLOELDLSGTLVLPPEALL 300

DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSLOELDLSGTLVLPPEALL 300

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

DB 301 HLPALQSVGVQDVCRCRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL 353

QY 126 ESTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRLVHPTRAGIPART 185  
 DB 145 EFTSSPLSDINSHNRLEVSISAFRTTSSQGRALHVDLSHNLRLHPARASIPART 204  
 QY 186 IQLNLAMNRLHVPNLRDPLRYSLSDGNPLAVIGPGAFAGLGLTTHSLASLQRLPEL 245  
 DB 205 IQLNLAMNRLHVPNLRDPLRYSLSDGNPLAVIGPGAFAGLGLTTHSLASLQRLPEL 264  
 QY 246 APGFGFRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHLPL 305  
 DB 265 PPHGFGFRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHLPL 324  
 QY 306 QSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTL 353  
 DB 325 QSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTL 372

## RESULT 4

Q9UG10 PRELIMINARY; PRT; 242 AA.

AC Q9UG10; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP586E011.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Kocher K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL110276; CAB53711.1; -  
 DR PIR; T14791; T14791.  
 DR InterPro; IPR001611; LRR.  
 DR Pfam; PF00560; LRR; 3.  
 DR Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 242 AA; 25835 MW; 66C51DB722ACECA2 CRC64;

Query Match 67.6%; Score 1235; DB 4; Length 242;  
 Best Local Similarity 99.6%; Pred. No. 2,4e-87;  
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 112 SLDISHNGTLALPESPTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRL 171  
 DB 1 SLDISHNGTLALPESPTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRL 60  
 QY 172 LVHPTRAGIPARTIQLNLAMNRLHVPNLRDPLRYSLSDGNPLAVIGPGAFAGLGL 231  
 DB 61 LVHPTRAGIPARTIQLNLAMNRLHVPNLRDPLRYSLSDGNPLAVIGPGAFAGLGL 120  
 QY 232 THSLASLQRLPELAPGFGFRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNL 291  
 DB 121 THSLASLQRLPELAPGFGFRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNL 180  
 QY 292 VPLPEALLHLPLALQSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPT 351  
 DB 181 VPLPEALLHLPLALQSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPT 240  
 QY 352 IL 353  
 DB 241 IL 242

## RESULT 5

Q7ZUT1 PRELIMINARY; PRT; 347 AA.  
 ID Q7ZUT1  
 AC Q7ZUT1;

DT 01-JUN-2003 (TREMblrel. 24, Created)  
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Body;  
 RA Strausberg R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC047843; AA447843.1; -  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003591; LRR\_TYP.  
 DR Pfam; PF00560; LRR; 6.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00366; LRR\_PS; 4.  
 DR SMART; SM00369; LRR\_TYP; 6.  
 DR Hypothetical protein.  
 SQ SEQUENCE 347 AA; 37775 MW; 1EB5446DD0871B80 CRC64;

Query Match 42.0%; Score 767; DB 13; Length 347;  
 Best Local Similarity 49.6%; Pred. No. 4.7e-51;  
 Matches 168; Conservative 48; Mismatches 109; Indels 14; Gaps 5;

QY 6 LLLAVASGQTRRCPCGCEVEFTFGLPDSFLTRDCSGLGHMPVPIPLDTAHL 65  
 DB 11 LLGLAALCA--VKNCHQRCREVEFTFGLPDSFLTKDCRIGGNRPVPIPLDTSHLD 68  
 QY 66 SSNRIEMWESVLAPGTYTLAGLDSHNLTSISPAFSLRYLBSLDSHNGLTPLA 125  
 DB 69 SLNSTTSSIDTMSLGGPTTLVSLDLSNNIAQISPAFSLRYLFTLDSNNALBGLSD 128  
 QY 126 ESFTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNL--THRLVP--HPTAGL 181  
 DB 129 GCFGLPFLVELDLSNQKFNLDLFTTRTODLPIMVDSLRLTSLFRRTPGHPL---- 184  
 QY 182 PAPTIQSLNLMNRLHVPNLRDPLRYSLSDGNPLAVIGPGAFAGLGLTHSLASLQRL 241  
 DB 185 --YKSLMLAGNGLKTPKRLNGIPQLYLNLDGNLSSITGAFDSLTBLVHLSLSGLSE 241  
 QY 242 LPELAPGFGFRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHL 301  
 DB 242 LTLHPGAFRSLKVLQALDLSNNSQLKTLNPNVPSGLVSLQELNLSNTAATVPLSRIVFMQ 301  
 QY 302 LPAQSVSVGDVRCRLVREGTYPRRPG--SSPKVPLHC 339  
 DB 302 MPNIKSLTLPNVHCKWTHMGQGFHRQIGAKPNDILTC 340

## RESULT 6

Q8N182 PRELIMINARY; PRT; 713 AA.

AC Q8N182; 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Glioma amplified on chromosome 1 protein (leucine-rich).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034047; AA434047.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; Ig-like.



DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR007110; Ig\_1like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00560; LRR; 10.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_Typ; 1.  
 DR PROSITE; PS50835; Ig\_Like; 1.  
 DR Immunoglobulin domain; Signal.  
 KM SIGNAL 1 20  
 PT CHAIN 21 >707  
 PT NON\_TER 707 707  
 SQ SEQUENCE 707 AA; 79156 MW; FAETC1573DD165B CRC64;

Query Match 14.3%; Score 261; DB 11; Length 707;  
 Best Local Similarity 25.9%; Pred. No. 1.3e-11;  
 Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

QY 24 CQCEVETFGLEFDSFSL--TRVDSGLGPHIMVPVPIPLDTAHLDLSSRLMENVESVLAP 81  
 DB 33 CTCEIRPWFPTPSIYMASVTDCCNDGLNFPALPADTQILLLQTNVNIARIEHST--D 89  
 QY 82 GYTLGAGLDLSHNLTSISPTAFRLRYLESIDLSHNGLTALPAES--FTSSPLSDVNL 140  
 DB 90 FPNVLTGLDLSQNNLSVTNINQKMSQLSVLEENKLTLPKCLYGLSNLQELVNH 149  
 QY 141 NQLEEVSAFTTHSQGRALHVD-----LSHNLHRL----- 172  
 DB 150 NLSTISPGAFIGLHNLRLHLNSNRLQMINSCWFDALPNLEILMGLDNPRIIRKDNFQ 209  
 QY 173 -----VPHPTAGLPARTIOSLNLAMNRLHAVENL---RDLPLRYLSL 212  
 DB 210 PLVKRLSVIAGINLLEIPDDALAGL--ENLESISFYDNRLSKVPQVALOKAVNLKFLDL 267  
 QY 213 DGNPLAVIGPAGFAGLGLTHLSLASLQRLPELAPSGFRELPGLQVLDLSGNPKLWAGA 272  
 DB 268 NKNPINIRRGDFSNMLHKLGINNPELVISIDSLAVDNLPLRKIEATNPNRLSYIHP 327  
 QY 273 EVFSGLSLQELDLSGTVLVPLEALLHLPALQSVV--QGVRCRLVR---EGTYPR 327  
 DB 328 NAFRLPLGLSILMNTNALSALVHGTTESLPNLKEISHSNPTRCDVCVIRIMNKTNIIR 387  
 QY 328 --RPGSPKVPPLHCVDTRE 344  
 DB 388 FMEPDS-----LFCVDPPE 401

## RESULT 9

O8CB6 PRELIMINARY; PRT; 707 AA.  
 AC O8CB6;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Leucine rich repeat protein 3.  
 GN LRN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CK NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=22354683; PubMed=1246851;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 AT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK036316; BAC29381.1; -  
 DR MGI; MGI:106036; Lrrn3.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003599; Ig\_III.  
 DR InterPro; IPR007110; Ig\_1like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00560; LRR; 10.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS50835; Ig\_Like; 1.  
 SQ SEQUENCE 707 AA; 79175 MW; DFCAG09A2553E0FC CRC64;

Query Match 14.3%; Score 261; DB 11; Length 707;  
 Best Local Similarity 25.9%; Pred. No. 1.3e-11;  
 Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

QY 24 CQCEVETFGLEFDSFSL--TRVDSGLGPHIMVPVPIPLDTAHLDLSSRLMENVESVLAP 81  
 DB 33 CTCEIRPWFPTPSIYMASVTDCCNDGLNFPALPADTQILLLQTNVNIARIEHST--D 89  
 QY 82 GYTLGAGLDLSHNLTSISPTAFRLRYLESIDLSHNGLTALPAES--FTSSPLSDVNL 140  
 DB 90 FPNVLTGLDLSQNNLSVTNINQKMSQLSVLEENKLTLPKCLYGLSNLQELVNH 149  
 QY 141 NQLEEVSAFTTHSQGRALHVD-----LSHNLHRL----- 172  
 DB 150 NLSTISPGAFIGLHNLRLHLNSNRLQMINSCWFDALPNLEILMGLDNPRIIRKDNFQ 209  
 QY 173 -----VPHPTAGLPARTIOSLNLAMNRLHAVENL---RDLPLRYLSL 212  
 DB 210 PLVKRLSVIAGINLLEIPDDALAGL--ENLESISFYDNRLSKVPQVALOKAVNLKFLDL 267  
 QY 213 DGNPLAVIGPAGFAGLGLTHLSLASLQRLPELAPSGFRELPGLQVLDLSGNPKLWAGA 272  
 DB 268 NKNPINIRRGDFSNMLHKLGINNPELVISIDSLAVDNLPLRKIEATNPNRLSYIHP 327  
 QY 273 EVFSGLSLQELDLSGTVLVPLEALLHLPALQSVV--QGVRCRLVR---EGTYPR 327  
 DB 328 NAFRLPLGLSILMNTNALSALVHGTTESLPNLKEISHSNPTRCDVCVIRIMNKTNIIR 387  
 QY 328 --RPGSPKVPPLHCVDTRE 344  
 DB 388 FMEPDS-----LFCVDPPE 401

## RESULT 10

O8CB7 PRELIMINARY; PRT; 363 AA.  
 AC O8CB7;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE G protein-coupled receptor 49.  
 GN GPR49.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=22354683; PubMed=12466851;
RX THE FANTOM Consortium,
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK047873; BAC3180.1; -
DR MGI; MGI:1341817; Gpr49.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR_9.
DR Pfam; PF01462; LRRNT_1.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00013; LRRNT; 1.
SQ SEQUENCE 363 AA; 39880 MW; DSE2FC4449FCB2C0 CRC64;

Query Match 14.1%; Score 258; DB 11; Length 363;
Best Local Similarity 29.8%; Pred. No. 8.9e-12;
Matches 89; Conservative 40; Mismatches 104; Indels 66; Gaps 9;

OY 6 LLLAVSGAQ-----TRPCPPGQCCEVEFPGLFDFSFSLTFVDCSGLPHIMPVPIPLDT 60
DB 15 LLLAVSGSPGPAIPRGCPSHCHCEL-----DGRYLKLVDCSDGLSELPSNLVSFT 68
OY 61 AHDLSRRLMEVSVIAGPYTTIAGLDSHNLISISTASRLRYLESIDLNSHGL 120
DB 69 SYLLSNMNIISQLPASLL-----HRCFLKXLRLAGNAL 102
OY 121 TALPAESPT-SPLSDVNLSHNOLREVSFAFTTHSQGRALHVDLSHNLHRLVPHPTRA 179
DB 103 THIRKATGLHSLKVLMLQNNQRLQVPEELQNLRSQSLRLDANH--ISYVPS---- 156
OY 180 GLPAPTIOGLNLMNRLHAVNRLDPLRYISLDGNPLAVIGPAFAGLGGTLHSLASL 239
DB 157 -----CSGGLHS-----LRHMLDNLALDVPVQAFRSLSLAQMTLA-L 195
OY 240 QRLPELAPSGFRELPGLOVLDLSDGNPKLMWAGAEVFGSLSGELSDGTNLVPLPEAL 298
DB 196 NKIHILADYAFGNLSLVVLHLHNN-RHISLCKKCFDGLHSLFTLDLANNVLDSEPTAI 253

RESULT 11
O9H3W5 PRELIMINARY; PRT; 708 AA.
AC O9H3W5; O43377;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Neuronal leucine-rich repeat protein-3)
DE (Leucine-rich repeat protein).
GN DKFZP761K2424 OR NLR-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weill B., Wiemann S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hamano S., Inuzuka H., Morohashi A., Ohira M., Nakagawara A.;
RT "Human neuronal leucine-rich repeat protein-3 (NLR-3).";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Jin L., Yu L., Zhao S.Y.;

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RT "Cloning of a new human cDNA homologous to Mus musculus leucine-rich
   repeat protein.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL442092; CAC09450.1; -
DR EMBL; AB060967; BAB47184.1; -
DR EMBL; AF134481; AAP97258.1; -
DR Genew; HGNC:17200; LRRN3.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig_IIIc.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00041; fn3_1.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00560; LRR_9.
DR Pfam; PF01463; LRRCT_1.
DR Pfam; PF01462; LRRNT_1.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00060; FN3_1.
DR SMART; SM00408; Ig_c2_1.
DR SMART; SM00082; LRRCT_1.
DR SMART; SM00013; LRRNT_1.
DR SMART; SM00369; LRR_cyp_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 708 AA; 79424 MW; 24710478DEB124D1 CRC64;

Query Match 13.9%; Score 254; DB 4; Length 708;
Best Local Similarity 25.1%; Pred. No. 4.4e-11;
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

OY 24 CCEVEFTGLFDFSPSL-----TRVDCSGLPHIMPVPIPLDTAHLDSRLMEVSVIA 79
DB 33 CTEIRPW--FPRRSYMEASTVDCNDLGLTFEPALPANTQILLQTNIAKIE----- 85
OY 80 GPGYTT-----LAGLDSHNLISPTAFSLRYLESIDLNSHGLTALPASSFTS-SPL 133
DB 86 ---YSTDFPNVNLGLDLSNNLSSVTINVKKPOLLSYLEENKLTPEKCLSLSLNL 142
OY 134 SDVNLSHNOLREVSFAFTTHSQGRALHYD-----LSHNLIR 171
DB 143 GEIYINHLNSTISPAFGLHNLRLHLSNRLQWINSKWPDALPNEIIMIGEPIIR 202
OY 172 L-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?- 205
DB 203 IKDMNFKPLINLSLVIAGINLLEIPDNALVGL--ENLESISFYDRLIKVPHVALQKV 260
OY 206 PLRYISLDGNPLAVIGPAFAGLGLTHLSIASLQRLPELAPSGFRELPGLOVLDLSDNP 265
DB 261 NLFFLDLKNKPIRIKRGPSNMLHKEIGINMPETISIDSLAVDNLDPDKIKETATNP 320
OY 266 KLMWAGAEVFGSLSGELSDGTNLVPLPEALLLTPALQSVSV-GQDVRGRRLYR--- 321
DB 321 RLSEYHPNAPFRLPKLESIMLSNLSALYHGHTIESLPMLKEISHSNIRCDVCVIRWNN 380
OY 322 -EGTYPR--RPGSSPKVPLHCVDTRE 344
DB 381 MNKTIIRFMEPDS-----LPCVDPP 401

RESULT 12
O24250 PRELIMINARY; PRT; 733 AA.
AC O24250;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE TARTAN protein precursor.
GN TRN OR CG11280.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

[illegible]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:02:32 ; Search time 54 Seconds

(Without alignments)  
1847.024 Million cell updates/sec

Title: US-10-017-390A-397  
Perfect score: 1828  
Sequence: 1 MPWPLLLLVSGAQTTRPC.....KVPILHCVDTRSNARGPITL 353

Scoring table: BIOSIM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1828	100.0	353	3	AB24026 Human PRO
2	1828	100.0	353	4	AAV99455 Human PRO
3	1828	100.0	353	4	AA66204 Human PRO
4	1828	100.0	353	6	ABO33697 Novel hum
5	1828	100.0	353	7	ABO44550 Human sec
6	1828	100.0	353	7	ABO33574 Novel hum
7	1828	100.0	353	7	ADCI18266 Human PRO
8	1828	100.0	353	7	ADCI18266 Human PRO
9	1828	100.0	353	7	ADCI18266 Human PRO
10	1828	100.0	353	7	ADCI18266 Human PRO
11	1828	100.0	353	7	ADCI18266 Human PRO
12	1828	100.0	353	7	ADCI18266 Human PRO
13	1828	100.0	353	7	ADCI18266 Human PRO
14	1828	100.0	353	7	ADCI18266 Human PRO
15	1828	100.0	353	7	ADCI18266 Human PRO
16	1828	100.0	353	7	ADCI18266 Human PRO
17	1828	100.0	353	7	ADCI18266 Human PRO
18	1828	100.0	353	7	ADCI18266 Human PRO
19	1828	100.0	353	7	ADCI18266 Human PRO
20	1828	100.0	353	7	ADCI18266 Human PRO
21	1828	100.0	353	7	ADCI18266 Human PRO
22	1828	100.0	353	7	ADCI18266 Human PRO
23	1828	100.0	353	7	ADCI18266 Human PRO
24	1828	100.0	353	7	ADCI18266 Human PRO
25	1828	100.0	353	7	ADCI18266 Human PRO

26	1813	99.2	353	5	AB663352 Human alb
27	1813	99.2	353	5	AB663352 Human alb
28	1798	95.1	337	7	ABO32590 Secreted
29	1636	89.5	321	7	AB664350 Human PRO
30	1623.5	88.8	357	3	AB640712 Human ORF
31	1048	57.3	200	6	ABO32591 Secreted
32	578	31.6	114	6	ABO32593 Secreted
33	318.5	17.4	713	2	AAV13385 Amino aci
34	318.5	17.4	713	3	ADCI18266 Human PRO
35	318.5	17.4	713	4	ADCI18266 Human PRO
36	318.5	17.4	713	6	ADCI18266 Human PRO
37	318.5	17.4	713	6	ADCI18266 Human PRO
38	318.5	17.4	713	6	ADCI18266 Human PRO
39	318.5	17.4	713	6	ADCI18266 Human PRO
40	318.5	17.4	713	6	ADCI18266 Human PRO
41	318.5	17.4	713	6	ADCI18266 Human PRO
42	318.5	17.4	713	6	ADCI18266 Human PRO
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46	318.5	17.4	713	6	ADCI18266 Human PRO
47	318.5	17.4	713	6	ADCI18266 Human PRO
48	318.5	17.4	713	6	ADCI18266 Human PRO
49	318.5	17.4	713	6	ADCI18266 Human PRO
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98	318.5	17.4	713	6	ADCI18266 Human PRO

99	267.5	14.6	673	4	AA87533	112	267.5	14.6	673	7	ADD07351	ADD0351	Novel hum
100	267.5	14.6	673	4	AA86516	113	267.5	14.6	673	7	ADD82242	ADD82242	Human PRO
101	267.5	14.6	673	5	AAU75266	114	267.5	14.6	673	7	ADD08422	ADD08422	Human PRO
102	267.5	14.6	673	5	AB935858	115	267.5	14.6	673	7	ADD06671	ADD06671	Novel hum
103	267.5	14.6	673	5	AB878042	116	267.5	14.6	673	7	ADD82918	ADD82918	Human PRO
104	267.5	14.6	673	6	ABU57981	117	267.5	14.6	673	7	ADD55025	ADD55025	Human PRO
105	267.5	14.6	673	6	ABU59059	118	267.5	14.6	673	7	ADD36020	ADD36020	Novel hum
106	267.5	14.6	673	6	ABU82571	119	267.5	14.6	673	7	ADD55983	ADD55983	Human PRO
107	267.5	14.6	673	6	ABU60490	120	267.5	14.6	673	7	ADD54421	ADD54421	Human PRO
108	267.5	14.6	673	6	ABU72457	121	267.5	14.6	673	7	ADD26575	ADD26575	Novel hum
109	267.5	14.6	673	6	ABU72457	122	267.5	14.6	673	8	ADD26042	ADD26042	Novel hum
110	267.5	14.6	673	6	ABU90883	123	267.5	14.6	673	8	ADD58154	ADD58154	Novel hum
111	267.5	14.6	673	6	ABO33942	124	267.5	14.6	673	3	AA838400	AA838400	Fragment
112	267.5	14.6	673	6	ABU71959	125	266	14.6	673	7	AB85589	AB85589	Novel hum
113	267.5	14.6	673	6	ABU71513	126	265.5	14.5	673	7	AB85506	AB85506	Human sec
114	267.5	14.6	673	6	ABU72294	127	265.5	14.5	692	2	AAU93340	AAU93340	Human nov
115	267.5	14.6	673	6	ABU90967	128	265	14.5	692	2	AAW93890	AAW93890	Human HG3
116	267.5	14.6	673	6	ABU59206	129	265	14.5	907	3	AAW93889	AAW93889	Human HG3
117	267.5	14.6	673	6	ABO55903	130	265	14.5	907	3	AAW90682	AAW90682	Human G P
118	267.5	14.6	673	6	ABO27288	131	265	14.5	907	3	AAW90687	AAW90687	Human mut
119	267.5	14.6	673	6	ABU92483	132	265	14.5	907	6	ABP81968	ABP81968	Human G-P
120	267.5	14.6	673	6	ABO81153	133	265	14.5	907	7	ABO06467	ABO06467	Human G-P
121	267.5	14.6	673	6	ABO53268	134	265	14.5	907	7	ADCC2797	ADCC2797	Human G P
122	267.5	14.6	673	6	ABU58912	135	265	14.5	907	7	ADCC2783	ADCC2783	Human G P
123	267.5	14.6	673	6	ABU52290	136	265	14.5	907	7	ADCC2783	ADCC2783	Human G P
124	267.5	14.6	673	6	ABU59355	137	265	14.5	907	7	ADCC2783	ADCC2783	Human G P
125	267.5	14.6	673	6	ABU98270	138	262	14.3	949	2	AAW93904	AAW93904	Human AOM
126	267.5	14.6	673	6	ABU99275	139	262	14.3	949	2	AAW93905	AAW93905	Human AOM
127	267.5	14.6	673	6	ABU82482	140	262	14.3	951	2	AAW93965	AAW93965	Human AOM
128	267.5	14.6	673	6	ABU92121	141	262	14.3	951	2	AAW92835	AAW92835	Human AOM
129	267.5	14.6	673	6	ABU96446	142	262	14.3	951	4	AAE22835	AAE22835	Human AOM
130	267.5	14.6	673	6	ABU10827	143	262	14.3	951	4	AAE22835	AAE22835	Human AOM
131	267.5	14.6	673	6	ABU81516	144	262	14.3	951	4	AAU32972	AAU32972	Novel hum
132	267.5	14.6	673	6	ABU72116	145	261	14.3	951	4	AAE03524	AAE03524	Human sec
133	267.5	14.6	673	6	ABU88518	146	256	14.0	951	2	AAO30403	AAO30403	Human IGR
134	267.5	14.6	673	6	ABO34032	147	256	14.0	951	5	ABE05224	ABE05224	Human IGR
135	267.5	14.6	673	6	ABD17073	148	256	14.0	951	2	ABE5116	ABE5116	Novel hum
136	267.5	14.6	673	6	ADA37563	149	255.5	14.0	794	4	AAE82352	AAE82352	Human IGR
137	267.5	14.6	673	6	ADA21249	150	255.5	14.0	794	4	AAE45513	AAE45513	Human IGR
138	267.5	14.6	673	6	ABO44246	151	254	13.9	705	3	AAE03600	AAE03600	Human IGR
139	267.5	14.6	673	6	ADA10036	152	254	13.9	705	3	AAE45513	AAE45513	Human IGR
140	267.5	14.6	673	6	ADA19878	153	254	13.9	705	3	AAE78823	AAE78823	Human IGR
141	267.5	14.6	673	6	ADA17261	154	254	13.9	708	2	AAE78823	AAE78823	Human IGR
142	267.5	14.6	673	6	ADA17580	155	254	13.9	708	2	AAE78823	AAE78823	Human IGR
143	267.5	14.6	673	6	ADA27688	156	254	13.9	708	2	AAE78823	AAE78823	Human IGR
144	267.5	14.6	673	6	ADA27688	157	254	13.9	708	2	AAE78823	AAE78823	Human IGR
145	267.5	14.6	673	6	ADA20050	158	254	13.9	708	2	AAE78823	AAE78823	Human IGR
146	267.5	14.6	673	6	ABO34174	159	254	13.9	708	2	AAE78823	AAE78823	Human IGR
147	267.5	14.6	673	6	ADA34258	160	254	13.9	708	2	AAE78823	AAE78823	Human IGR
148	267.5	14.6	673	6	ADA38493	161	254	13.9	708	2	AAE78823	AAE78823	Human IGR
149	267.5	14.6	673	6	ADA26214	162	254	13.9	708	2	AAE78823	AAE78823	Human IGR
150	267.5	14.6	673	6	ADA00347	163	254	13.9	708	2	AAE78823	AAE78823	Human IGR
151	267.5	14.6	673	7	ABO53118	164	254	13.9	708	2	AAE78823	AAE78823	Human IGR
152	267.5	14.6	673	7	ABO53118	165	254	13.9	708	2	AAE78823	AAE78823	Human IGR
153	267.5	14.6	673	7	ABO53118	166	254	13.9	708	2	AAE78823	AAE78823	Human IGR
154	267.5	14.6	673	7	ABO53118	167	254	13.9	708	2	AAE78823	AAE78823	Human IGR
155	267.5	14.6	673	7	ABO53118	168	254	13.9	708	2	AAE78823	AAE78823	Human IGR
156	267.5	14.6	673	7	ABO53118	169	254	13.9	708	2	AAE78823	AAE78823	Human IGR
157	267.5	14.6	673	7	ABO53118	170	254	13.9	708	2	AAE78823	AAE78823	Human IGR
158	267.5	14.6	673	7	ABO53118	171	254	13.9	708	2	AAE78823	AAE78823	Human IGR
159	267.5	14.6	673	7	ABO53118								
160	267.5	14.6	673	7	ABO53118								
161	267.5	14.6	673	7	ABO53118								
162	267.5	14.6	673	7	ABO53118								
163	267.5	14.6	673	7	ABO53118								
164	267.5	14.6	673	7	ABO53118								
165	267.5	14.6	673	7	ABO53118								
166	267.5	14.6	673	7	ABO53118								
167	267.5	14.6	673	7	ABO53118								
168	267.5	14.6	673	7	ABO53118								
169	267.5	14.6	673	7	ABO53118								
170	267.5	14.6	673	7	ABO53118								
171	267.5	14.6	673	7	ABO53118								

245	254	13.9	708	6	ADB29274	AdB29274	Human	sec	318	254	13.9	708	7	ADB38038	AdB38038	Novel	hum
246	254	13.9	708	6	ADA18898	Ada18898	Human	PRO	319	254	13.9	708	7	ADB66510	AdB66510	Novel	hum
247	254	13.9	708	6	ADA61521	Ada61521	Homo	sapi	320	254	13.9	708	7	ADB89590	AdB89590	Human	PRO
248	254	13.9	708	6	ADB19306	AdB19306	Novel	hum	321	254	13.9	708	7	ADB90332	AdB90332	Human	PRO
249	254	13.9	708	6	ADB27847	AdB27847	Human	PRO	322	254	13.9	708	7	ADB77595	AdB77595	Human	sec
250	254	13.9	708	6	ADA86326	Ada86326	Novel	hum	323	254	13.9	708	7	ADB39423	AdB39423	Novel	hum
251	254	13.9	708	6	ADB15890	AdB15890	Human	PRO	324	254	13.9	708	7	ADB74731	AdB74731	Human	sec
252	254	13.9	708	6	ADA47676	Ada47676	Human	PRO	325	254	13.9	708	7	ADB47046	AdB47046	Novel	hum
253	254	13.9	708	6	ADA18130	Ada18130	Human	sec	326	254	13.9	708	7	ADB66553	AdB66553	Human	PRO
254	254	13.9	708	6	ABO32767	AbO32767	Human	sec	327	254	13.9	708	7	ADB77258	AdB77258	Novel	hum
255	254	13.9	708	6	ADA67471	Ada67471	Human	PRO	328	254	13.9	708	7	ADB34415	AdB34415	Human	PRO
256	254	13.9	708	6	ADB30478	AdB30478	Human	PRO	329	254	13.9	708	7	ADB35519	AdB35519	Human	PRO
257	254	13.9	708	6	ADA85774	Ada85774	Novel	hum	330	254	13.9	708	7	ADB33863	AdB33863	Human	PRO
258	254	13.9	708	6	ADA96986	Ada96986	Human	PRO	331	254	13.9	708	7	ADB34967	AdB34967	Human	PRO
259	254	13.9	708	6	ADA79290	Ada79290	Human	PRO	332	254	13.9	708	7	ADB36071	AdB36071	Human	PRO
260	254	13.9	708	6	ADA87429	Ada87429	Novel	hum	333	254	13.9	708	7	ADB46466	AdB46466	Novel	hum
261	254	13.9	708	6	ADB16631	AdB16631	Human	PRO	334	254	13.9	708	7	ADB28377	AdB28377	Human	sec
262	254	13.9	708	6	ABO34827	AbO34827	Human	PRO	335	254	13.9	708	7	ADC39577	AdC39577	Human	sec
263	254	13.9	708	6	ADA16105	Ada16105	Human	sec	336	254	13.9	708	7	ADC40091	AdC40091	Human	sec
264	254	13.9	708	6	ADA91723	Ada91723	Novel	hum	337	254	13.9	708	7	ADC18919	AdC18919	Human	sec
265	254	13.9	708	6	ADB14786	AdB14786	Human	PRO	338	254	13.9	708	7	ADC34215	AdC34215	Human	sec
266	254	13.9	708	6	ADB18747	AdB18747	Novel	hum	339	254	13.9	708	7	ADC29270	AdC29270	Human	sec
267	254	13.9	708	6	ADA93962	Ada93962	Human	PRO	340	254	13.9	708	7	ADC28801	AdC28801	Human	sec
268	254	13.9	708	6	ADB19858	AdB19858	Novel	hum	341	254	13.9	708	7	ADC40686	AdC40686	Human	sec
269	254	13.9	708	6	ADB13170	AdB13170	Human	PRO	342	254	13.9	708	7	ADC19343	AdC19343	Human	sec
270	254	13.9	708	6	ABO43297	AbO43297	Novel	hum	343	254	13.9	708	7	ADC33791	AdC33791	Human	sec
271	254	13.9	708	6	ADA74424	Ada74424	Human	PRO	344	254	13.9	708	7	ADC12861	AdC12861	Human	sec
272	254	13.9	708	6	ADA42250	Ada42250	Human	sec	345	254	13.9	708	7	ADC50339	AdC50339	Novel	hum
273	254	13.9	708	6	ADB24657	AdB24657	Human	PRO	346	254	13.9	708	7	ADC71886	AdC71886	Novel	hum
274	254	13.9	708	6	ADA82181	Ada82181	Human	PRO	347	254	13.9	708	7	ADC59865	AdC59865	Novel	hum
275	254	13.9	708	6	ADA75144	Ada75144	Human	PRO	348	254	13.9	708	7	ADC52872	AdC52872	Novel	hum
276	254	13.9	708	6	ADA85222	Ada85222	Novel	hum	349	254	13.9	708	7	ADC57226	AdC57226	Novel	hum
277	254	13.9	708	6	ADA84670	Ada84670	Novel	hum	350	254	13.9	708	7	ADC60417	AdC60417	Novel	hum
278	254	13.9	708	6	ABO17505	AbO17505	Human	PRO	351	254	13.9	708	7	ADC50892	AdC50892	Novel	hum
279	254	13.9	708	6	ADB29926	AdB29926	Human	PRO	352	254	13.9	708	7	ADC65419	AdC65419	Human	PRO
280	254	13.9	708	6	ADA80454	Ada80454	Human	PRO	353	254	13.9	708	7	ADC54517	AdC54517	Novel	hum
281	254	13.9	708	6	ADA75696	Ada75696	Human	PRO	354	254	13.9	708	7	ADC53478	AdC53478	Novel	hum
282	254	13.9	708	6	ADA46921	Ada46921	Human	PRO	355	254	13.9	708	7	ADC59001	AdC59001	Novel	hum
283	254	13.9	708	6	ADB25217	AdB25217	Human	PRO	356	254	13.9	708	7	ADC55879	AdC55879	Novel	hum
284	254	13.9	708	6	ADA93393	Ada93393	Human	PRO	357	254	13.9	708	7	ADC58449	AdC58449	Novel	hum
285	254	13.9	708	6	ADB26743	AdB26743	Human	PRO	358	254	13.9	708	7	ADC12313	AdC12313	Human	sec
286	254	13.9	708	6	ADB31030	AdB31030	Human	PRO	359	254	13.9	708	7	ADDD03123	AdD03123	Human	sec
287	254	13.9	708	6	ADA60958	Ada60958	Homo	sapi	360	254	13.9	708	7	ADC90115	AdC90115	Novel	hum
288	254	13.9	708	6	ADB24105	AdB24105	Human	PRO	361	254	13.9	708	7	ADC69534	AdC69534	Human	PRO
289	254	13.9	708	6	ADA96434	Ada96434	Human	PRO	362	254	13.9	708	7	ADC48423	AdC48423	Human	PRO
290	254	13.9	708	6	ADA81006	Ada81006	Human	PRO	363	254	13.9	708	7	ADC09952	AdC09952	Human	PRO
291	254	13.9	708	6	ADA95882	Ada95882	Human	PRO	364	254	13.9	708	7	ADDD04527	AdD04527	Novel	hum
292	254	13.9	708	6	ADB26191	AdB26191	Human	PRO	365	254	13.9	708	7	ADC80483	AdC80483	Novel	hum
293	254	13.9	708	6	ADB21676	AdB21676	Novel	hum	366	254	13.9	708	7	ADDD10990	AdD10990	Human	PRO
294	254	13.9	708	7	ADA77455	Ada77455	Human	PRO	367	254	13.9	708	7	ADC47871	AdC47871	Human	PRO
295	254	13.9	708	7	ADB18195	AdB18195	Human	PRO	368	254	13.9	708	7	ADDD04868	AdD04868	Human	sec
296	254	13.9	708	7	ADA86878	Ada86878	Novel	hum	369	254	13.9	708	7	ADC79931	AdC79931	Novel	hum
297	254	13.9	708	7	ADA16529	Ada16529	Human	sec	370	254	13.9	708	7	ADDD09400	AdD09400	Human	PRO
298	254	13.9	708	7	ADA12958	Ada12958	Human	sec	371	254	13.9	708	7	ADDD03874	AdD03874	Human	sec
299	254	13.9	708	7	ADA41826	Ada41826	Human	sec	372	254	13.9	708	7	ADDD03450	AdD03450	Human	sec
300	254	13.9	708	7	ADA87981	Ada87981	Novel	hum	373	254	13.9	708	7	ADDD41113	AdD41113	Novel	hum
301	254	13.9	708	7	ADA45369	Ada45369	Novel	hum	374	254	13.9	708	7	ADDD52252	AdD52252	Human	PRO
302	254	13.9	708	7	ADA17173	Ada17173	Human	sec	375	254	13.9	708	7	ADDD52992	AdD52992	Human	PRO
303	254	13.9	708	7	ADA42676	Ada42676	Human	sec	376	254	13.9	708	7	ADDD53544	AdD53544	Novel	hum
304	254	13.9	708	7	ADB28399	AdB28399	Human	PRO	377	254	13.9	708	7	ADDD51700	AdD51700	Human	PRO
305	254	13.9	708	7	ADB28951	AdB28951	Human	PRO	378	254	13.9	708	7	ADDD02499	AdD02499	Human	PRO
306	254	13.9	708	7	ADA76903	Ada76903	Human	PRO	379	254	13.9	708	7	ADDD01933	AdD01933	Human	PRO
307	254	13.9	708	7	ADA86533	Ada86533	Novel	hum	380	254	13.9	708	7	ADDD54115	AdD54115	Novel	hum
308	254	13.9	708	7	ADA97538	Ada97538	Human	PRO	381	254	13.9	708	7	ADDD92432	AdD92432	Human	PRO
309	254	13.9	708	7	ADB27295	AdB27295	Human	PRO	382	254	13.9	708	7	ADDD91328	AdD91328	Human	PRO
310	254	13.9	708	7	ADB22228	AdB22228	Novel	hum	383	254	13.9	708	7	ADDE03942	AdE03942	Human	PRO
311	254	13.9	708	7	ABO17566	AbO17566	Human	PRO	384	254	13.9	708	7	ADDE32239	AdE32239	Novel	hum
312	254	13.9	708	7	ADA66919	Ada66919	Human	PRO	385	254	13.9	708	7	ADDE22171	AdE22171	Human	PRO
313	254	13.9	708	7	ADB22780	AdB22780	Human	PRO	386	254	13.9	708	7	ADDD79395	AdD79395	Human	PRO
314	254	13.9	708	7	ADB23553	AdB23553	Human	PRO	387	254	13.9	708	7	ADDE41931	AdE41931	Human	PRO
315	254	13.9	708	7	ADA92275	Ada92275	Novel	hum	388	254	13.9	708	7	ADDE17748	AdE17748	Human	PRO
316	254	13.9	708	7	ADB15338	AdB15338	Human	PRO	389	254	13.9	708	7	ADDD91880	AdD91880	Human	PRO
317	254	13.9	708	7	ADB38590	AdB38590	Novel	hum	390	254	13.9	708	7	ADDE33343	AdE33343	Novel	hum

391	254	13.9	708	7	ADB33895	Adg33895	Novel hum
392	254	13.9	708	7	ADD79947	Add79947	Human PRO
393	254	13.9	708	7	ADD92984	Add92984	Human PRO
394	254	13.9	708	7	ADB19404	Adel19404	Human PRO
395	254	13.9	708	7	ADB34702	Adel34702	Human sec
396	254	13.9	708	7	ADB18952	Adel18952	Human PRO
397	254	13.9	708	7	ADB33048	Adel33048	Human PRO
398	254	13.9	708	7	ADB58587	Adel58587	Human PRO
399	254	13.9	708	7	ADB22723	Adel22723	Human PRO
400	254	13.9	708	7	ADB78841	Adel78841	Human PRO
401	254	13.9	708	7	ADB32791	Adel32791	Novel hum
402	254	13.9	708	7	ADB32483	Adel32483	Human PRO
403	254	13.9	708	7	ADB80499	Adel80499	Human PRO
404	254	13.9	708	7	ADB89537	Adel89537	Human PRO
405	254	13.9	708	7	ADB40811	Adel40811	Human PRO
406	254	13.9	708	7	ADB04610	Adel04610	Human PRO
407	254	13.9	708	8	ADB81035	Adel81035	Novel hum
408	254	13.9	708	8	ADB79147	Adel79147	Human sec
409	254	13.9	708	8	ADB76483	Adel76483	Human PRO
410	254	13.9	708	8	ADB76483	Adel76484	Human PRO
411	254	13.9	708	8	ADB86251	Adel86251	Human PRO
412	254	13.9	708	8	ADB79571	Adel79571	Human sec
413	254	13.9	708	8	ADB75699	Adel75699	Human PRO
414	254	13.9	708	8	ADB73247	Adel73247	Human sec
415	254	13.9	708	8	ADB23275	Adel23275	Human PRO
416	254	13.9	708	8	ADB23827	Adel23827	Human PRO
417	254	13.9	708	8	ADB24470	Adel24470	Human PRO
418	254	13.9	708	8	ADB87295	Adel87295	Human PRO
419	254	13.9	708	8	ADB89161	Adel89161	Human PRO
420	254	13.9	708	8	ADB73762	Adel73762	Human sec
421	254	13.9	708	8	ADB18300	Adel18300	Human PRO
422	254	13.9	708	8	ADB88609	Adel88609	Human PRO
423	254	13.9	708	8	ADB85608	Adel85608	Drosophila
424	252	13.8	719	4	AAW79807	Aaw79807	Human PRO
425	252	13.8	719	4	AAW41095	Aaw41095	Human PRO
426	252	13.7	347	4	AAW5074	Aaw5074	Human PRO
427	250	13.7	347	4	AAW03823	Aaw03823	Human PRO
428	250	13.7	347	4	AAW03848	Aaw03848	Human PRO
429	250	13.7	347	4	AAW03849	Aaw03849	Human PRO
430	250	13.7	347	4	AAW33983	Aaw33983	Human PRO
431	250	13.7	347	5	ABG64524	Abg64524	Human alb
432	250	13.7	347	5	ABG64525	Abg64525	Human alb
433	250	13.7	347	5	ABG64525	Abg64525	Human alb
434	250	13.7	347	5	ABG64525	Abg64525	Human alb
435	249	13.6	951	6	ABU19812	Abu19812	Androgen
436	249	13.6	951	6	ABP81676	Abp81676	Human G P
437	248.5	13.6	630	5	AAU75267	Aau75267	Human S11
438	248	13.6	347	3	AAW71108	Aaw71108	Human Hyd
439	248	13.6	347	6	ABR43442	Abi43442	Human mal
440	248	13.6	347	6	ABR43429	Abi43429	Human mal
441	248	13.6	347	6	ABR43430	Abi43430	Human mal
442	247.5	13.5	493	3	AAW07431	Aaw07431	A leucine
443	247.5	13.5	673	5	ABG78046	Abg78046	Mouse leu
444	247.5	13.5	560	2	AAW71294	Aaw71294	Human gly
445	247	13.5	560	3	AAV69184	Aav69184	Amino aci
446	247	13.5	560	3	AAU78892	Aau78892	Human end
447	247	13.5	560	4	ABW63571	Abw63571	Drosophila
448	246.5	13.5	707	2	AAU02379	Aau02379	Polypept
449	245.5	13.4	1300	4	ABW64083	Abw64083	Drosophila
450	245	13.4	605	4	AAW65892	Aaw65892	Amino aci
451	245	13.4	673	6	ADA00753	Ada00753	Murine st
452	244.5	13.3	673	6	ABW64950	Abw64950	Gene 11 h
453	243.5	13.3	1513	4	ABW71361	Abw71361	Drosophila
454	240	13.1	578	7	ADCB8708	Adcb8708	Rat leuci
455	239.5	13.1	312	3	AAW41795	Aaw41795	Human ORF
456	239	13.1	967	5	AAW66138	Aaw66138	Mouse IGR
457	238.5	13.0	312	4	AAW03882	Aaw03882	Human gen
458	238.5	13.0	344	4	AAW40351	Aaw40351	Human pol
459	238.5	13.0	352	4	ABG22569	Abg22569	Novel hum
460	238.5	13.0	379	2	AAW17820	Aaw17820	Human PRO
461	238.5	13.0	379	2	AAW17820	Aaw17820	Human PRO
462	238.5	13.0	379	2	AAW17820	Aaw17820	Human PRO
463	238.5	13.0	379	4	AAU12335	Aau12335	Human PRO

464	238.5	13.0	379	5	ABW4831	Abw4831	Human PRO
465	238.5	13.0	379	5	ABW5437	Abw5437	Human PRO
466	238.5	13.0	379	6	ABW5920	Abw5920	Human sec
467	238.5	13.0	379	6	ABW17779	Abw17779	Novel hum
468	238.5	13.0	379	6	ABW02230	Abw02230	Human PRO
469	238.5	13.0	379	6	ABW01033	Abw01033	Human PRO
470	238.5	13.0	379	6	ABW4916	Abw4916	Human sec
471	238.5	13.0	379	6	ABW67733	Abw67733	Human PRO
472	238.5	13.0	379	6	ABW58350	Abw58350	Novel hum
473	238.5	13.0	379	6	ABW57236	Abw57236	Human PRO
474	238.5	13.0	379	6	ABW59814	Abw59814	Novel sec
475	238.5	13.0	379	6	ABW025004	Abw025004	Human sec
476	238.5	13.0	379	6	ABW06301	Abw06301	Human sec
477	238.5	13.0	379	6	ABW67009	Abw67009	Human sec
478	238.5	13.0	379	6	ABW11302	Abw11302	Human PRO
479	238.5	13.0	379	6	ABW67121	Abw67121	Human PRO
480	238.5	13.0	379	6	ABW45847	Abw45847	Novel hum
481	238.5	13.0	379	6	ADW476278	Adw476278	Human PRO
482	238.5	13.0	379	6	ADW418928	Adw418928	Human PRO
483	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
484	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
485	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
486	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
487	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
488	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
489	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
490	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
491	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
492	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
493	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
494	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
495	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
496	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
497	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
498	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
499	238.5	13.0	379	6	ADW41551	Adw41551	Novel hum
500	238.5	13.0	379	7	ADW41551	Adw41551	Novel hum

## ALIGNMENTS

## RESULT 1

ID AAB24026 standard; protein: 353 AA.

AAB24026; 25-JAN-2001 (first entry)

Human PRO1788 protein sequence SEQ IDNO:18.

Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumorigenesis; anticancer; detection.

Homo sapiens.

MO200053750-AL.

14-SEP-2000.

02-DEC-1999; 99WO-US028551.

08-MAR-1999; 99WO-US005028.

01-SEP-1999; 99WO-US020111.

29-OCT-1998; 98US-0162506P.

30-NOV-1999; 99WO-US028313.

01-DEC-1999; 99WO-US028634.

(GETH ) GENENTECH INC.

Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

DR WPI; 2000-594320/56.  
 DR N-PSDB; AAC58108.  
 XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
 PT the growth of tumors in mammals, and to identify inhibitors of PRO  
 FT polypeptide activity or expression.  
 XX  
 PS Claim 61; Fig 12; 226pp; English.  
 XX  
 CC The present invention describes an antibody that binds to a human protein  
 CC (1) selected from: PRO181; PRO1269; PRO1410; PRO1755; PRO1780; PRO1434;  
 CC PRO1927; PRO1567; PRO1295; PRO1283; PRO1303; PRO1444; PRO1554; PRO1397;  
 CC PRO1407; PRO1555; PRO1096; PRO2038; and PRO2262. (1) has anticancer  
 CC activity and can be used to diagnose tumors in mammals, by detecting  
 CC complex formation when the antibody is contacted with test cells.  
 CC Increased expression of genes encoding (1) can also be detected to  
 CC diagnose tumors. Agents which inhibit the activity of (1), especially  
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes  
 CC encoding (1), can be used to inhibit tumour growth, preferably by  
 CC inducing cell death. Methods from the present invention can be used to  
 CC identify compounds which inhibit the biological activity of (1). AAC58019  
 CC to AAC58102 represent PCR primers and hybridisation probes used in  
 CC examples from the present invention for human PRO sequences. AAC58103 to  
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and  
 CC protein sequences given in the exemplification of the present invention  
 XX  
 SQ Sequence 353 AA:  
 Query Match 100.0%; Score 1828; DB 3; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 PD 09-MAR-2000.  
 XX  
 PF 01-SEP-1999;  
 XX 99WO-US020111.  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099356P.  
 PR 09-SEP-1998; 98US-0099398P.  
 PR 09-SEP-1998; 98US-0099602P.  
 PR 09-SEP-1998; 98US-0099642P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099754P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099808P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 10-SEP-1998; 98US-0099815P.  
 PR 10-SEP-1998; 98US-0099816P.  
 PR 15-SEP-1998; 98US-0100385P.  
 PR 15-SEP-1998; 98US-0100388P.  
 PR 15-SEP-1998; 98US-0100390P.  
 PR 16-SEP-1998; 98US-0100584P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100661P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 16-SEP-1998; 98US-0100664P.  
 PR 17-SEP-1998; 98US-0100683P.  
 PR 17-SEP-1998; 98US-0100684P.  
 PR 17-SEP-1998; 98US-0100710P.  
 PR 17-SEP-1998; 98US-0100711P.  
 PR 17-SEP-1998; 98US-0100919P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 18-SEP-1998; 98US-0100848P.  
 PR 18-SEP-1998; 98US-0100849P.  
 PR 18-SEP-1998; 98US-0101014P.  
 PR 18-SEP-1998; 98US-0101068P.  
 PR 18-SEP-1998; 98US-0101071P.  
 PR 22-SEP-1998; 98US-0101279P.  
 PR 23-SEP-1998; 98US-0101471P.  
 PR 23-SEP-1998; 98US-0101472P.  
 PR 23-SEP-1998; 98US-0101473P.  
 PR 23-SEP-1998; 98US-0101474P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 23-SEP-1998; 98US-0101476P.  
 PR 23-SEP-1998; 98US-0101477P.  
 PR 23-SEP-1998; 98US-0101479P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101741P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 24-SEP-1998; 98US-0101915P.  
 PR 24-SEP-1998; 98US-0101916P.  
 PR 29-SEP-1998; 98US-0102070P.  
 PR 29-SEP-1998; 98US-0102400P.  
 PR 29-SEP-1998; 98US-0102307P.  
 PR 29-SEP-1998; 98US-0102330P.  
 PR 29-SEP-1998; 98US-0102331P.  
 PR 30-SEP-1998; 98US-0102484P.  
 PR 30-SEP-1998; 98US-0102487P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 30-SEP-1998; 98US-0102571P.  
 PR 01-OCT-1998; 98US-0102684P.  
 PR 01-OCT-1998; 98US-0102687P.  
 PR 01-OCT-1998; 98US-0102689P.  
 PR 06-OCT-1998; 98US-0103258P.  
 PR 06-OCT-1998; 98US-0103499P.  
 PR 07-OCT-1998; 98US-0103314P.  
 PR 07-OCT-1998; 98US-0103315P.  
 PR 07-OCT-1998; 98US-0103328P.

RESULT 2  
 AAY99455  
 ID AAY99455 standard; protein; 353 AA.  
 XX  
 AC AAY99455;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Human PRO1788 (UNQ850) amino acid sequence SEQ ID NO:397.  
 XX  
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
 OS Homo sapiens.  
 XX  
 XX  
 FN WO200012708-A2.





XX WPI: 2001-071395/08.  
 DR Secreted and transmembrane proteins and nucleic acids designated PRO.  
 XX PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 PT  
 XX Claim 1; Fig 232; 787bp; English.  
 PS  
 XX The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 CC  
 XX Sequence 353 AA:  
 SO  
 Query Match 100.0%; Score 1828; DB 4; Length 353;  
 Best local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MPWPLLLLAASGQTRPCPGCCGCEVETFGFLDSFSLRVDCSGLGPPIHMPYPIPLDT 60  
 Db 1 MPWPLLLLAASGQTRPCPGCCGCEVETFGFLDSFSLRVDCSGLGPPIHMPYPIPLDT 60  
 Cy 61 AHDLSNRLEMVESVLAGPGYTTLAGLDLSHNLTSISPTASRLRYLESIDLSHNGL 120  
 Db 61 AHDLSNRLEMVESVLAGPGYTTLAGLDLSHNLTSISPTASRLRYLESIDLSHNGL 120  
 Cy 121 TALPASEFTSSPLSDVLSHQLEEVSAFTTISQGRALHVDLSHNLIRLVPHPRAG 180  
 Db 121 TALPASEFTSSPLSDVLSHQLEEVSAFTTISQGRALHVDLSHNLIRLVPHPRAG 180  
 Cy 181 LPAPTISQINLAKRILHVPNLRLPLRYLSLDGNPLAVGPGAFIGGTHLSLASLQ 240  
 Db 181 LPAPTISQINLAKRILHVPNLRLPLRYLSLDGNPLAVGPGAFIGGTHLSLASLQ 240  
 Cy 241 RLPELARGPREFLPGLQVLDLSGNPKLNAGAEVFGSLGSLQELDLSGTMVLPPEALL 300  
 Db 241 RLPELARGPREFLPGLQVLDLSGNPKLNAGAEVFGSLGSLQELDLSGTMVLPPEALL 300  
 Cy 301 HLPALQSVSGQDYRCRLVREGTYPPRPSSGPVPLHCVTRRSAAAGPTIL 353  
 Db 301 HLPALQSVSGQDYRCRLVREGTYPPRPSSGPVPLHCVTRRSAAAGPTIL 353

RESULT 4  
 ABO33697  
 ID ABO33697 standard; protein; 353 AA.  
 XX  
 AC ABO33697;  
 XX  
 DT 17-SEP-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO1788.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;  
 KW endothelial cell proliferation; wound healing; immune response;  
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
 KW cardiac insufficiency disorder; calcium flux; inflammation;  
 KW vascular endothelial growth factor-stimulated proliferation;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;  
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;  
 KW pancreatic beta-cell precursor cell differentiation; thalassemia;  
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
 KW cartilage disorder; sports injury; arthritis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2003073130-A1.  
 PN

XX PD 17-APR-2003.  
 XX  
 XX 11-DEC-2001. 2001US-00015869.  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098723P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 03-SEP-1998; 98US-0098936P.  
 PR 03-SEP-1998; 98US-0098956P.  
 PR 03-SEP-1998; 98US-0098958P.  
 PR 03-SEP-1998; 98US-00989602P.  
 PR 09-SEP-1998; 98US-0098942P.  
 PR 10-SEP-1998; 98US-0098941P.  
 PR 10-SEP-1998; 98US-0098954P.  
 PR 10-SEP-1998; 98US-00989763P.  
 PR 10-SEP-1998; 98US-00989792P.  
 PR 10-SEP-1998; 98US-00989808P.  
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 PR 10-SEP-1998; 98US-00989815P.  
 PR 10-SEP-1998; 98US-00989816P.  
 PR 15-SEP-1998; 98US-0100385P.  
 PR 15-SEP-1998; 98US-0100388P.  
 PR 15-SEP-1998; 98US-0100390P.  
 PR 16-SEP-1998; 98US-0100584P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100661P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 16-SEP-1998; 98US-0100664P.  
 PR 17-SEP-1998; 98US-0100683P.  
 PR 17-SEP-1998; 98US-0100684P.  
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 PR 17-SEP-1998; 98US-0100711P.  
 PR 17-SEP-1998; 98US-0100919P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 18-SEP-1998; 98US-0100848P.  
 PR 18-SEP-1998; 98US-0100849P.  
 PR 18-SEP-1998; 98US-0101014P.  
 PR 18-SEP-1998; 98US-0101068P.  
 PR 18-SEP-1998; 98US-0101071P.  
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 PR 30-SEP-1998; 98US-0102487P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 30-SEP-1998; 98US-0102571P.  
 PR 01-OCT-1998; 98US-0102684P.  
 PR 01-OCT-1998; 98US-0102687P.  
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 PR 06-OCT-1998; 98US-0103258P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 07-OCT-1998; 98US-0103314P.  
 PR 07-OCT-1998; 98US-0103315P.  
 PR 07-OCT-1998; 98US-0103328P.

PR 07-OCT-1998; 98US-0103395P.  
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 PR 07-OCT-1998; 98US-0103401P.  
 PR 08-OCT-1998; 98US-0103533P.  
 PR 08-OCT-1998; 98US-0103678P.  
 PR 08-OCT-1998; 98US-0103679P.  
 PR 14-OCT-1998; 98US-0104257P.  
 PR 20-OCT-1998; 98US-0104987P.  
 PR 20-OCT-1998; 98US-0105000P.  
 PR 20-OCT-1998; 98US-0105002P.  
 PR 21-OCT-1998; 98US-0105104P.  
 PR 22-OCT-1998; 98US-0105169P.  
 PR 22-OCT-1998; 98US-0105266P.  
 PR 26-OCT-1998; 98US-0105693P.  
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 PR 27-OCT-1998; 98US-0105807P.  
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 PR 28-OCT-1998; 98US-0106030P.  
 PR 28-OCT-1998; 98US-0106032P.  
 PR 28-OCT-1998; 98US-0106033P.  
 PR 28-OCT-1998; 98US-0106178P.  
 PR 29-OCT-1998; 98US-0106248P.  
 PR 29-OCT-1998; 98US-0106384P.  
 PR 29-OCT-1998; 98US-0108500P.  
 PR 30-OCT-1998; 98US-0106464P.  
 PR 03-NOV-1998; 98US-0106856P.  
 PR 03-NOV-1998; 98US-0106902P.  
 PR 03-NOV-1998; 98US-0106905P.  
 PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
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 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
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 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 30-DEC-1998; 98US-0114223P.  
 PR 05-JAN-1999; 99US-US000106.  
 PR 16-APR-1999; 99US-0129674P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99US-US020111.  
 PR 15-SEP-1999; 99US-US021194.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99US-US028313.  
 PR 02-DEC-1999; 99US-US028551.  
 PR 16-DEC-1999; 99US-US030095.  
 PR 05-JAN-2000; 2000US-US000219.  
 PR 06-JAN-2000; 2000US-US000376.  
 PR 11-FEB-2000; 2000US-US003565.  
 PR 18-FEB-2000; 2000US-US004342.  
 PR 24-FEB-2000; 2000US-US005004.  
 PR 02-MAR-2000; 2000US-US005841.

PR 15-MAR-2000; 2000US-US006884.  
 PR 17-MAY-2000; 2000US-US013705.  
 PR 22-MAY-2000; 2000US-US014042.  
 PR 30-MAY-2000; 2000US-US014941.  
 PR 02-JUN-2000; 2000US-US015264.  
 PR 23-AUG-2000; 2000US-US023522.  
 PR 24-AUG-2000; 2000US-US023328.  
 PR 08-NOV-2000; 2000US-US030952.  
 PR 10-NOV-2000; 2000US-US030873.  
 PR 01-DEC-2000; 2000US-US032678.  
 PR 28-FEB-2001; 2001US-US006520.  
 PR 01-MAR-2001; 2001US-US006666.  
 PR 01-JUN-2001; 2001US-US017800.  
 PR 20-JUN-2001; 2001US-US019692.  
 PR 29-JUN-2001; 2001US-US021066.  
 PR 09-JUL-2001; 2001US-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Fan J, Fagan NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams EM, Wood WI;  
 XX  
 XX MPI; 2003-585293/55.  
 DR N-PSDB; ACD68519.  
 XX  
 XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,  
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal  
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-  
 Query Match 100.0%; Score 1828; DB 6; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPWLLILAVSGAQTTRPCPPGQCEVETFGLEFDSSTLRVDCSGGPHIMVPIPLDT 60  
 DB 1 MPWLLILAVSGAQTTRPCPPGQCEVETFGLEFDSSTLRVDCSGGPHIMVPIPLDT 60  
 QY AHDLSNRLEMNESVLAGPGYTTLAGLDSHNLTSISPTAFSRLRYLESIDLSHNGL 120  
 DB 61 AHDLSNRLEMNESVLAGPGYTTLAGLDSHNLTSISPTAFSRLRYLESIDLSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNISHNQLREVSVSAFTTHSQGRALHVDLSHNLIRLVHPTRAG 180  
 DB 121 TALPAESFTSSPLSDVNISHNQLREVSVSAFTTHSQGRALHVDLSHNLIRLVHPTRAG 180  
 QY 181 LPAPTOSINAMRIHAPVLRDPLRYSLDGNPLAVIGPAGLGGTHTLSIASLQ 240  
 DB 181 LPAPTOSINAMRIHAPVLRDPLRYSLDGNPLAVIGPAGLGGTHTLSIASLQ 240  
 QY 241 RLPELAPSGFRELPGQLVLDLSGNPKLNMAGAEVFSGLSLQELDLSGTNLVPLPEALL 300  
 DB 241 RLPELAPSGFRELPGQLVLDLSGNPKLNMAGAEVFSGLSLQELDLSGTNLVPLPEALL 300  
 QY 301 HLPALQSVGQDVACRLVREGTYPRRPGSSPVPLVCVTRTSAAAGPTIL 353  
 DB 301 HLPALQSVGQDVACRLVREGTYPRRPGSSPVPLVCVTRTSAAAGPTIL 353  
 RESULT 5  
 ID ABO44550  
 ID ABO44550 standard; protein; 353 AA.  
 XX ABO44550;  
 AC  
 XX  
 XX  
 DT 01-OCT-2003 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1788.  
 XX  
 XX Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;  
 KW antidiabetic; anorectic; antiarthritis; angiogenesis; cancer;

KW adrenal cortical capillary; endothelial cell growth; wound healing;  
KW stimulated T-lymphocyte proliferation; immune response suppression;  
KW neonatal heart hypertrophy; cardiac insufficiency disorder;  
KW vascular endothelial growth factor; inflammation; mononuclear cell;  
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;  
KW sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2003044841-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006856.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099536P.  
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PR 20-JUN-2001; 2001MO-US019692.
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PR 09-JUL-2001; 2001MO-US021735.

XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desroyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ;
PI Pan U, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI: 2003-585292/55.
XX N-PSDB; ACD68165.
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic vaccines.
XX Claim 12; Fig 232; 561pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
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 XX  
 XX (GENTH ) GENENTECH INC.  
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 PI Baker KP, Botstein D, Desnoyers L, Batton DJ, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Pecht NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
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 XX WPI; 2003-555602/52.  
 DR N-PSDB; ADC18265.  
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 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.  
 XX  
 XX Claim 12; SEQ ID NO 397; 555pp; English.  
 XX  
 XX The invention relates to human PRO polypeptides and the polynucleotides  
 XX encoding them. The sequences are useful in the preparation of a  
 XX medicament for treating a condition responsive to a PRO polypeptide. The  
 XX polypeptides are useful in a number of functional biological assays, as  
 XX molecular weight markers for protein electrophoresis and as therapeutic  
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 Best Local Similarity 100.0%; Pred. No. 1.se-167;

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 DT XX  
 DT 15-JAN-2004 (first entry)  
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 DE XX  
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 KW Immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
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 OS Homo sapiens.  
 OS XX  
 PN US2003099625-A1.  
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XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S,  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
PI Williams FM, Wood WI;  
XX



DR WPI; 2003-874602/81.  
 DR N-PSDB; ADD70911.  
 XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.  
 PT  
 PS Claim 12; SEQ ID NO 397; 553bp; English.  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167; Indels 0; Gaps 0;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9  
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 KM Human; secreted protein; transmembrane protein; PRO; tumour;  
 KM immune response; cardiac insufficiency disorder; calcium flux;  
 KM umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KM arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KM Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KM dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
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 PN US2003083462-A1.  
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 PD 01-MAY-2003.  
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 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021056.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GENENTECH INC.  
 XX  
 PI Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wacanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-755122/71.  
 DR N-PSDB; ADD39988.  
 XX  
 PT New secreted and transmembrane PRO polypeptides useful for treating  
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or  
 PT hypo-insulinemia, sports injuries and arthritis.  
 XX  
 PS Claim 12; SEQ ID NO 397; 553bp; English.  
 XX

The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 123 fully defined sequences as given in the specification (including their extracellular domains either or without their associated signal peptides). Also include are the CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a host cell comprising the vector, producing PRO, a chimeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO is useful as molecular weight markers for protein electrophoresis and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is useful for generating transgenic animals or knock-out animals which are CC useful in gene development and screening useful reagents. PRO NA is also useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are useful for treating cancerous tumours. PRO1550, PRO1418 and PRO1410 polypeptides are useful for suppressing immune response. PRO1246 polypeptide is useful for treating cardiac insufficiency disorders. PRO1246 polypeptide is also useful for treating tumours. PRO1246 and PRO1561 polypeptide are useful for stimulating calcium flux in human umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474 polypeptides are useful for treating bone and/or cartilage disorders (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating Berger disease or other nephropathies associated with Schonlein-Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1418, PRO1410 and PRO1575 are useful in treating thalassemias. The present sequence represents a PRO protein of the invention.

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWLLLLAVGAGCTTTPCPCGCCCEVEVTFGLFDSFSLTRVDCSGLGPHIMFVPIPDT 60  
Db 1 MPWLLLLAVGAGCTTTPCPCGCCCEVEVTFGLFDSFSLTRVDCSGLGPHIMFVPIPDT 60

QY 61 AHLDLSSNRLIEMVNESVLAGPGYTTLAGIDLSHNLITSISPAFSPRLRLIESLDSHNL 120  
Db 61 AHLDLSSNRLIEMVNESVLAGPGYTTLAGIDLSHNLITSISPAFSPRLRLIESLDSHNL 120

QY 121 TALPASFTSPSPSDVNLISHNOLREVSVAFTTSSQGRALHYDLSHNLHRLVPHPTAG 180  
Db 121 TALPASFTSPSPSDVNLISHNOLREVSVAFTTSSQGRALHYDLSHNLHRLVPHPTAG 180

QY 181 LPAFTIQTINLAWNRLLHAYPNLRDLPLRYLSLDGNPLAVIGCAFAIGLGLTHLSIASIQ 240  
Db 181 LPAFTIQTINLAWNRLLHAYPNLRDLPLRYLSLDGNPLAVIGCAFAIGLGLTHLSIASIQ 240

QY 241 RLPELAPSGRRLPGIQTIDISGNPKLWAGAEVFSGLSLQELDLSGTNLVLPBALIL 300  
Db 241 RLPELAPSGRRLPGIQTIDISGNPKLWAGAEVFSGLSLQELDLSGTNLVLPBALIL 300

QY 301 HLPALQSVSGQDVRCRLVREGTYPRRGSSPKVBLHCVDTRESAARGPTIL 353  
Db 301 HLPALQSVSGQDVRCRLVREGTYPRRGSSPKVBLHCVDTRESAARGPTIL 353

RESULT 10  
ADD70435  
ID ADD70435 standard; protein; 353 AA.  
XX  
AC ADD70435;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
KW Humane; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; neuropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
PN US2003054406-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006818.  
XX

PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100380P.  
PR 16-SEP-1998; 98US-0100884P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 17-SEP-1998; 98US-0100931P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 22-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
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PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
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PR 02-OCT-1998; 98US-0102685P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-0103314P.  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103356P.  
PR 07-OCT-1998; 98US-0103356P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.

PR 28-OCT-1998; 98US-0106178P.  
 PR 29-OCT-1998; 98US-0106248P.  
 PR 29-OCT-1998; 98US-0106384P.  
 PR 29-OCT-1998; 98US-0108300P.  
 PR 30-OCT-1998; 98US-0106464P.  
 PR 03-NOV-1998; 98US-0106856P.  
 PR 03-NOV-1998; 98US-0106902P.  
 PR 03-NOV-1998; 98US-0106905P.  
 PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
 PR 17-NOV-1998; 98US-0108788P.  
 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108867P.  
 PR 18-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 PR 22-DEC-1998; 98US-0113286P.  
 PR 30-DEC-1998; 98US-0114223P.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 16-APR-1999; 99US-0129674P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021194.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Bolstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski J, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paout NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI,  
 XX

DR WPI; 2003-708344/67.  
 DR N-PSDB; ADD70434.  
 XX  
 PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
 PT biological activity of cell, as molecular weight markers in protein  
 PT electrophoresis, for treating arthritis, tumor.  
 XX  
 XX Claim 12; SEQ ID NO 397; 549pp; English.  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEMPLLLLAAGCAQTRPCFCGCEVEETGFLFDSFELTRVDCSGLSPHMPVPIPDT 60  
 DB 1 MEMPLLLLAAGCAQTRPCFCGCEVEETGFLFDSFELTRVDCSGLSPHMPVPIPDT 60  
 QY 61 AHDLSNRLKLVNNSVLAGPGYTTLAGLDLSHNLITISPTAFRLKYLSSLDLSHNL 120  
 DB 61 AHDLSNRLKLVNNSVLAGPGYTTLAGLDLSHNLITISPTAFRLKYLSSLDLSHNL 120  
 QY 121 TALPASFTSPSLDVNLSHNLREVSAFTTHSQGALHVDLSHNLHRLVPRPTAG 180  
 DB 121 TALPASFTSPSLDVNLSHNLREVSAFTTHSQGALHVDLSHNLHRLVPRPTAG 180  
 QY 181 LPAPTQSLNLAHNLHVAHPNLRDPLRYLSIDGNPLAVIGGAPAGLGGTLHSLAQ 240  
 DB 181 LPAPTQSLNLAHNLHVAHPNLRDPLRYLSIDGNPLAVIGGAPAGLGGTLHSLAQ 240  
 QY 241 RPELAPSGFRLPGQVTLDSGNPKLMAGAEVSSGSLQEDLSGTLVPEALL 300  
 DB 241 RPELAPSGFRLPGQVTLDSGNPKLMAGAEVSSGSLQEDLSGTLVPEALL 300  
 QY 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKYPLHCVDRRESAAGPTLL 353  
 DB 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKYPLHCVDRRESAAGPTLL 353  
 RESULT 11  
 ADD38556  
 ID ADD38556 standard; protein; 353 AA.  
 XX  
 AC ADD38556;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1788.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; celliac disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US2003096955-A1.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 07-DEC-2001; 2001US-00012755.  
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 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098723P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.

PR	09-SEP-1998;	98US-0099596P;
PR	09-SEP-1998;	98US-0099598P;
PR	09-SEP-1998;	98US-0099602P;
PR	09-SEP-1998;	98US-0099642P;
PR	10-SEP-1998;	98US-0099741P;
PR	10-SEP-1998;	98US-0099754P;
PR	10-SEP-1998;	98US-0099763P;
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PR	10-SEP-1998;	98US-0099808P;
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PR	15-SEP-1998;	98US-0100385P;
PR	15-SEP-1998;	98US-0100388P;
PR	15-SEP-1998;	98US-0100390P;
PR	16-SEP-1998;	98US-0100384P;
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PR	16-SEP-1998;	98US-0100662P;
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PR	17-SEP-1998;	98US-0100684P;
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PR	18-SEP-1998;	98US-0101014P;
PR	18-SEP-1998;	98US-0101068P;
PR	18-SEP-1998;	98US-0101071P;
PR	22-SEP-1998;	98US-0101279P;
PR	22-SEP-1998;	98US-0101471P;
PR	23-SEP-1998;	98US-0101472P;
PR	23-SEP-1998;	98US-0101475P;
PR	23-SEP-1998;	98US-0101476P;
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PR	24-SEP-1998;	98US-0101738P;
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PR	24-SEP-1998;	98US-0101915P;
PR	24-SEP-1998;	98US-0101918P;
PR	29-SEP-1998;	98US-0102207P;
PR	29-SEP-1998;	98US-0102240P;
PR	29-SEP-1998;	98US-0102307P;
PR	29-SEP-1998;	98US-0102330P;
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PR	30-SEP-1998;	98US-0102484P;
PR	30-SEP-1998;	98US-0102487P;
PR	30-SEP-1998;	98US-0102570P;
PR	30-SEP-1998;	98US-0102571P;
PR	01-OCT-1998;	98US-0102684P;
PR	01-OCT-1998;	98US-0102687P;
PR	02-OCT-1998;	98US-0102965P;
PR	06-OCT-1998;	98US-0103255P;
PR	06-OCT-1998;	98US-0103258P;
PR	07-OCT-1998;	98US-0103314P;
PR	07-OCT-1998;	98US-0103315P;
PR	07-OCT-1998;	98US-0103328P;
PR	07-OCT-1998;	98US-0103395P;
PR	07-OCT-1998;	98US-0103396P;
PR	07-OCT-1998;	98US-0103401P;
PR	08-OCT-1998;	98US-0103633P;
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PR	08-OCT-1998;	98US-0103711P;
PR	14-OCT-1998;	98US-0104257P;
PR	20-OCT-1998;	98US-0104897P;
PR	20-OCT-1998;	98US-0105000P;
PR	20-OCT-1998;	98US-0105002P;
PR	21-OCT-1998;	98US-0105104P;
PR	22-OCT-1998;	98US-0105169P;
PR	25-OCT-1998;	98US-0105266P;
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PR	26-OCT-1998;	98US-0105649P;
PR	27-OCT-1998;	98US-0105807P;
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PR	28-OCT-1998;	98US-0106032P;
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PR	28-OCT-1998;	98US-0106178P;
PR	29-OCT-1998;	98US-0106248P;
PR	29-OCT-1998;	98US-0106384P;
PR	29-OCT-1998;	98US-0106500P;
PR	30-OCT-1998;	98US-0106464P;
PR	03-NOV-1998;	98US-0106656P;
PR	03-NOV-1998;	98US-0106502P;
PR	03-NOV-1998;	98US-0106505P;
PR	03-NOV-1998;	98US-0106519P;
PR	03-NOV-1998;	98US-0106532P;
PR	03-NOV-1998;	98US-0106534P;
PR	03-NOV-1998;	98US-0107783P;
PR	17-NOV-1998;	98US-0108775P;
PR	17-NOV-1998;	98US-0108779P;
PR	17-NOV-1998;	98US-0108787P;
PR	17-NOV-1998;	98US-0108788P;
PR	17-NOV-1998;	98US-0108801P;
PR	17-NOV-1998;	

PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gueney AL, Hillan KJ,  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-787000/74.  
DR N-PSDB; ADD38555.  
XX  
PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,  
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,  
PT thalassemias.  
XX  
PS Claim 12; SEQ ID NO 397; 556BP; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity  
Query Match 100.0%; Score 1828; DB 7; Length 353;  
Best Local Similarity 100.0%; Pired. No. 1.5e-167; Mismatches 0; Gaps 0;  
Matches 353; Conservative 0; Indels 0;  
QY 1 MPFLLLLAVSGAQTTPCPGCGCEVETFGLEFDSFLRVDCSGIGPHMVPPLD 60  
Db 1 MPFLLLLAVSGAQTTPCPGCGCEVETFGLEFDSFLRVDCSGIGPHMVPPLD 60  
QY 61 AHDLSNRLEMVNESVLAGGCTTTAGLDSHNLISIEPTAFSRIRYESLDSHNL 120  
Db 61 AHDLSNRLEMVNESVLAGGCTTTAGLDSHNLISIEPTAFSRIRYESLDSHNL 120  
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Db 121 TALPAEFTSSPFLSDVNLSHQREVSVAFTTHSQGRALHVDLSHNLIRLVHPFRAG 180  
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Db 181 LPAPTQSINLAWNRHLAVPNLRDLPRLYSLDGNPLAVIGPAGLGGVTHLSASLQ 240  
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ID ADD39512 standard; protein; 353 AA.  
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AC ADD39512;  
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DT 15-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; tumor;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonelein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
XX  
OS Homo sapiens.  
XX  
FN US2003096954-A1.

XX 22-MAY-2003.  
PD 07-DEC-2001; 2001US-00011671.  
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PA		
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XX Human secreted/transmembrane protein PRO1788.  
DE  
XX  
XX Human; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpiformis; Crohn's disease; thalassemia.  
XX  
OS Homo sapiens.  
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XX US2003092061-A1.  
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XX 15-MAY-2003.  
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XX 06-DEC-2001; 2001US-00007194.  
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 PR 05-JAN-2000; 2000MO-US000219.  
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 PR 02-JUN-2000; 2000MO-US015264.  
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 PR 04-SEP-2001; 2001US-00946374.  
 (GENTH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan MJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-765477/72.  
 DR N-PSDB; ADD39034.

XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
 PT PRO124, PRO124, useful for treating cancerous tumors, cardiac  
 PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.

XX Claim 12; SEQ ID NO 397; 555bp; English.

XX The invention relates to an isolated PRO polypeptide (secreted or

XX Query March 100.0%; Score 1828; DB 7; Length 353;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-167; Mismatches 0; Gaps 0;

XX Matches 353; Conservative 0; Indels 0; Gaps 0;

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 DB 1 MPWELLLLVSAQOTTRPCFPQCQCEVETFGGLPDSFSLTRVDCSLGPHIMVPIPLDT 60  
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## RESULT 14

ID ADD40466 standard; protein; 353 AA.

AC ADD40466;

DT 15-JAN-2004 (first entry)

DE Human secreted/transmembrane protein PRO1788.

KW Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; neuropathy; Schönlein-Henoch purpura; celiac disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.

OS Homo sapiens.

PN US2003082627-A1.

FD 01-MAY-2003.

PF 06-DEC-2001; 2001US-00006117.

XX 01-SEP-1998; 98US-0098716P.  
 XX 01-SEP-1998; 98US-0098723P.  
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 XX 09-SEP-1998; 98US-0099602P.  
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 XX 10-SEP-1998; 98US-0099741P.  
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 XX 10-SEP-1998; 98US-0099763P.  
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 XX 15-SEP-1998; 98US-0100388P.  
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 XX 16-SEP-1998; 98US-0100584P.  
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XX (GETH ) GENENTECH INC.
XX Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Cao W, Goddard A, Godowski PJ, Grimaldi JC, Gutney AL, Hillan KJ,
PI Pan U, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK,
PI Williams PM, Wood WI;
DR MPI; 2003-755104/71.
XX N-PSDB; ADD40465.
XX
PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
XX insufficiency disorders.
XX
PS Claim 12; SEQ ID NO 397; 550bp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1828; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.5e-167;
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 PA (GETH ) GENENTECH INC.  
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 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI: 2003-708395/67.  
 DR N-PSDB: ADE50686.  
 PT Novel secreted and transmembrane PRO polypeptides useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 12: SEQ ID NO 397; 555pp; English.

XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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124	138.5	7.6	696	4	US-09-902-775A-91	Sequence 91, Appl	197	111.5	6	427	3	US-08-313-177-6	Sequence 4, Appl
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253	99	5.4	1144	1	US-08-261-663A-4	Sequence 4, Appli	326	91.5	5.0	415	4	US-09-252-991A-2392	Sequence 2392, A
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395 86 4.7 895 4 US-10-020-079-18 Sequence 18, Appl  
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478 82 4.5 347 4 US-09-252-991A-25150 Sequence 25150, A  
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480 82 4.5 425 3 US-08-462-467B-16 Sequence 16, Appl  
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490 82 4.5 1832 4 US-09-568-486-4 Sequence 4, Appl  
491 82 4.5 1832 4 US-09-568-472-4 Sequence 4, Appl  
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499 81.5 4.5 920 3 US-08-930-996A-8 Sequence 1, Appl  
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## ALIGNMENTS

US-09-907-794A-245  
; Sequence 245, Application US/09907794A  
; Patent No. 6635468  
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; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gutney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pau, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14



	Query Match	17.4%	Score 318.5	DB 4	Length 713	
	Best Local Similarity	27.6%	Fred. No. 3.3e-21			
	Matches 115	Conservative	55	Mismatches 161	Indels 85	Gaps 114
Qy	6	LILLAVSAQQT-----RCCFPCGCCCEVENFGFLGDFSP--SLTFVDCSGLGFHIMPVI	56			
	:   :   :		:   :   :			
Db	8	LILMAVAGATITVPYVPMWHPGPCPACCAQIAPWTFRSSRYEATIVDNCDELTVTPRAL	67			
	:   :   :		:   :   :			
Qy	57	PLDTAHLDLSSNRLEMVNESYLADPGY-TTLAGDLSHNLLTSISPTAFSRRLYDESIDL	115			
	:   :   :		:   :   :			
Db	68	PAGYTOLLGSNSIYRVDSGL---GYLANLTEDDLSGNSFDARDCCFFALPOLSLHL	124			
	:   :   :		:   :   :			
Qy	116	SHNGITALLPAESFTS-SPLSDVNLSHNOLEVSVAFTTHSQGRALHYDSLHTLRILVP	174			
	:   :   :		:   :   :			
Db	125	EENQITRLDEHSFAGLASLOELYNHNQLYRIAPARFGLNSTLIRLH--LNSNLURAI--	180			
	:   :   :		:   :   :			
Qy	175	HPTKRAQLPAPIQTQSANLAMNRLHAV-----PULRDL-----	205			
	:   :   :		:   :   :			
Db	181	-DSRFEMLPMLIEIMIGNKVDALIDMNFRELAPLARSLVLAKNNLRISDYALEGLOS	239			
	:   :   :		:   :   :			
Qy	206	-----PURYLSLDGPFLAVIGGAPAGGGTLTHSIASLQRLP	243			
	:   :   :		:   :   :			
Db	240	ESLSTYDNQLARVPRRALEQVPGFLFLDINKNPFLORVGEGDPANNALHKELGLNNMBELV	299			
	:   :   :		:   :   :			
Qy	244	ELAPSGFREILPGLQVLDLSGNFKLMAGAEVSGLSLOELDLSGTNVLPPEALLHLIP	303			
	:   :   :		:   :   :			
Db	300	SIDKRALVNLPELTLDITINNRRLSFIHPRATHHLPQWEETLMMNNALSALHQGVESLP	359			
	:   :   :		:   :   :			
Qy	304	ALQSVSV-GQDVRCRLVY-----EGTYPPRRGSSPKVPLHCVDTEE	344			
	:   :   :		:   :   :			

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Db          360 NLEQVEGLHGNPIRCDCAVIRMANNTGTRVAFIEPQSTLCAEPDLQRLPVREVPFRE 414
RESULT 2    US-09-905-125A-245
Sequence 245, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godowski, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin D.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423

```

SEQ ID NO 245  
 LENGTH: 713  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-905-125A-245

Query Match 17.4%; Score 318.5; DB 4; Length 713;  
 Best Local Similarity 27.6%; Pred. No. 3.3e-21;  
 Matches 115; Conservative 55; Mismatches 161; Indels 85; Gaps 11;

QY 6 LLLAVSGAQT-----RCPPGCCCEVETGGLDSF--SLTRVDCSGGPHMPVI 56  
 DB 8 LLLAVAGATATVPPVPMHVPCCPQCAQIRPMTSSRYEATTVDCNDLFTAVPPAL 67  
 QY 57 PLDTAHLDSNRLEWNEVESVLAGPGY-TTLAGLDSHNLITISPTAFSRLRYLESIDL 115  
 DB 68 PAGTQTLLOGNSIVRVDSGL--GYLANLTELDSQNSFSDARDCDFHALPQLLSLHL 124  
 QY 116 SHNGITLPAESFTS-SPLSDVNLSHNOLEVSVAFTTHSQGRLHVDLSHNLHRLVP 174  
 DB 125 EENQTLREDSFGLASLOELYLNHQLYRIAPRAFSGLSNLLRLH--LNSNLLRAI-- 180  
 QY 175 HPRAGLPARTIOSLNLAMRLHAV-----PNLRDL----- 205  
 DB 181 -DSRFEMLPNLIELMTGKGVDAIDMNFRLANLSRLVLAGNMLREISDYALEGQSL 239  
 QY 206 -----PLRYSLDGNPLAVIGPQAFAGLGLTHLSLASLQRLP 243  
 DB 240 ESLSFYDNLQARVPRALQVPGKFLDNLNKPLOQVGPQDFANMLHKLGLNNMBELV 299  
 QY 244 ELAPSGRELPGQLVLDLGNPKLNAGAEVFGSLSSLOSLDLSGNTNLPPLPALLHL 303  
 DB 300 SIDKALVNLBELTLDITNNPRLSFTHPRAFHLLPQMETLMMNNLSALHQQTVESLP 359  
 QY 304 ALQSVSV-GQDVRCRLVR-----EGTYPRRGGSPKYPPLHCVDTRE 344  
 DB 360 NLQEVGLHGNIRDCVIRMANATGTRVRFIEPOSTLCAEPDQLQRLPVREVPFRE 415

RESULT 3  
 US-09-902-775A-245  
 Sequence 245, Application US/09902775A  
 Patent No. 6686451  
 GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashtkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvarcoff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Macher, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20944  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 245  
 LENGTH: 713  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-902-775A-245

Query Match 17.4%; Score 318.5; DB 4; Length 713;  
 Best Local Similarity 27.6%; Pred. No. 3.3e-21;  
 Matches 115; Conservative 55; Mismatches 161; Indels 85; Gaps 11;

QY 6 LLLAVSGAQT-----RCPPGCCCEVETGGLDSF--SLTRVDCSGGPHMPVI 56  
 DB 8 LLLAVAGATATVPPVPMHVPCCPQCAQIRPMTSSRYEATTVDCNDLFTAVPPAL 67  
 QY 57 PLDTAHLDSNRLEWNEVESVLAGPGY-TTLAGLDSHNLITISPTAFSRLRYLESIDL 115  
 DB 68 PAGTQTLLOGNSIVRVDSGL--GYLANLTELDSQNSFSDARDCDFHALPQLLSLHL 124  
 QY 116 SHNGITLPAESFTS-SPLSDVNLSHNOLEVSVAFTTHSQGRLHVDLSHNLHRLVP 174  
 DB 125 EENQTLREDSFGLASLOELYLNHQLYRIAPRAFSGLSNLLRLH--LNSNLLRAI-- 180  
 QY 175 HPRAGLPARTIOSLNLAMRLHAV-----PNLRDL----- 205  
 DB 181 -DSRFEMLPNLIELMTGKGVDAIDMNFRLANLSRLVLAGNMLREISDYALEGQSL 239  
 QY 206 -----PLRYSLDGNPLAVIGPQAFAGLGLTHLSLASLQRLP 243  
 DB 240 ESLSFYDNLQARVPRALQVPGKFLDNLNKPLOQVGPQDFANMLHKLGLNNMBELV 299  
 QY 244 ELAPSGRELPGQLVLDLGNPKLNAGAEVFGSLSSLOSLDLSGNTNLPPLPALLHL 303  
 DB 300 SIDKALVNLBELTLDITNNPRLSFTHPRAFHLLPQMETLMMNNLSALHQQTVESLP 359  
 QY 304 ALQSVSV-GQDVRCRLVR-----EGTYPRRGGSPKYPPLHCVDTRE 344  
 DB 360 NLQEVGLHGNIRDCVIRMANATGTRVRFIEPOSTLCAEPDQLQRLPVREVPFRE 415

Query Match	14.5%;	Score 265;	DB 4;	Length 907;
Best Local Similarity	30.1%;	Pred. No. 5.	1e-16;	

Query Match	14.5%	Score 265	DB 4	Length 907
Best Local Similarity	30.1%	Pred. NC. 5.1e-16		
Matches	93	Conservative 32	Mismatches 102	Indels 82
				Gaps 9

  

QY	4	PLILLAVSQAQ-----	TTTPCFPGCGCEVEFFHGFDSFSRLRYDCSGAGPHIMPIPL	58
				:
DB	13	PVLQGLATGSSSRSGVLLRGCPTRHCEP-----	DERMLRVDCSDPLGSLFELPSLWS	66
				:
QY	59	DYAHLDISSNRLEMVNESVLAPGYTTTAGLDLSHNL	LTSSPTAFSRRLTESLDSH	118
				:
DB	67	FTSLYLDISMNN-----	ISQLLPNPLPSLRLEELRLAGN	100
				:
QY	119	GLTALPAPESFTS-SPLSDVNLSHNOLREVSAGFTTHSQGRALHVDLSHNLHRLVPHPT		177
				:
DB	101	ALTYTPRGATGTYGYSKVLMLQNNQIRHY-----	PT	131
				:
QY	178	RAGLPAPTIQSLNLMANRLHAAVNPTRDLP-----	LRVSLDGNPLAVIGPAGAFGLG	229
				:
DB	132	EALQNLRSLSQLRLDANHHSTYP-----	PSCSGLHSLRHMLMDNDNALTEIPVQAFRSL	186
				:
QY	230	GLTHLSIASIQRLPELAPSGFRELDELQYLDISGNPKLNMGAEVFSLSLSQSLDLSGT		289
				:
DB	187	ALQAMTLIA-LNKITHIIPDYAFGLSLVYLHLHNN-RHLSGKKCFDGLHLETLIDLNYN		244
				:
QY	290	NIVLPREAL		298

Db 245 NLDEPPTAI 253

RESULT 7  
US-09-131-648-2  
Sequence 2: Application US/09131648  
Patent No. 6168920  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Patterson, Chandra  
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS  
FILE REFERENCE: PP-0576 US  
CURRENT APPLICATION NUMBER: US/09/131,648  
CURRENT FILING DATE: 1998-08-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PERL Program  
SEQ ID NO 2  
LENGTH: 708  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: 2687731  
US-09-131-648-2

Query Match 13.9%; Score 254; DB 3; Length 708;  
Best Local Similarity 25.1%; Pred. No. 3.8e-15;  
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

QY 24 COCEVETFGLPDSFSL-----TRVDCSGLGPIMFVPIPLDTAHLDLSSNRLKLVNVSFLA 79  
DB 33 CTCEIRPW--FTPRSIWEASTVDCNDLGLTFPARLPANTQIILLQTNNAKIE----- 85  
QY 80 GPGYTT-----LAGLDLSHNLTSISPTASRLRYLESPLDSHNGITAPAESFTS--SPL 133  
DB 86 ---YSTDFPVNLGTGLDLSQNNLSSVNNINVKMPQLLSVYLEENKLTPEKCLSLSNL 142  
QY 134 SDVNLISNOLREVSASFTHSGQRAHVD-----LSHNLIR 171  
DB 143 QELVYNNHNLSTISPGAFGLHNLRLHLSNMLQMSKFPALPNLILMIGEPPIR 202  
QY 172 L-----VPHPTAGLPAPTIQSLANRLHAPVNL---RDL 205  
DB 203 IKDMFKPLINLSVIAGINLITEIPDNALVGL--ENLESISFYDNRLLIKVPRVALQXV 260  
QY 206 PLRYLSIDGPIPLAVIGGAFAGLGLTHLSLALQPLPAPSGFRELPGLOVLDLGNP 265  
DB 261 NLKFLDINKPINKIRRGDPSNMLHKEGGINNPPELISIDSLAVNLDPLKIEATNP 320  
QY 266 KLNWAGAEVFSGLSLQELDLSGNTLVLPBALLLHLPALQSVSV--GQDVRCRLVR-- 321  
DB 321 RLSTYIHNAFFRLPKLESIMLSNALSAALYHGITESLPNLKEISHSNPIRCDVCVRMWN 380  
QY 322 -EGYPR--RPGSPKPLKCVDTRE 344  
DB 381 MNTKNIREFMEPDS-----LFCVDPPE 401

RESULT 8  
US-09-907-794A-69  
Sequence 69: Application US/09907794A  
Patent No. 6635468  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gettsen, Mary B.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Machet, Jennie F.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,794A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 69  
LENGTH: 708  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-907-794A-69

Query Match 13.9%; Score 254; DB 4; Length 708;  
Best Local Similarity 25.1%; Pred. No. 3.8e-15;  
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;  
QY 24 COCEVETFGLPDSFSL-----TRVDCSGLGPIMFVPIPLDTAHLDLSSNRLKLVNVSFLA 79  
DB 33 CTCEIRPW--FTPRSIWEASTVDCNDLGLTFPARLPANTQIILLQTNNAKIE----- 85  
QY 80 GPGYTT-----LAGLDLSHNLTSISPTASRLRYLESPLDSHNGITAPAESFTS--SPL 133

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Db      86  ---YSTDFPVNLGDLDSQNNLSVTINVKKMPQLLSVLEENKLTPEKCLSELNLT 142
      134 SDVNLSHNOJREVSVSAFTTHSGRALHYD-----LSNHLIR 171
      143 QELVYNHMLSTISPGAFGLHNLRLHNSNRLQMINSKFDPALPNEILMGENPILR 202
      172 L-----VHPPTAGLPAPTIQSLNLANRHLAVPNL---RDL 205
      203 IKMNMKPLINRLSVIAGINLIEIDNALVGL--ENLSISFYDNRLIKVHVALQKV 260
      206 PLRYSLDGNPLAVIGPGAFAGLGLTHLSLASLQRLPELAFSGFRELPGLOVLDLGNP 265
      261 NLKFLDLNKNPILNIRRGDFSNMLHKELGINNMPELISDLSLVNLPDLRKIEATNTP 320
      266 KLMWAGAEVSG:SSIOELDLSGTNLVPLPEALLHLPALQSVY-GQDVRCRLVR--- 321
      321 RLSTYHNPAPFLPKLESLMNSNALSAHYGHTISLPLKELISHSNPIRCDVCIRMMN 380
      322 -EGTYPR--RPGSSPKVPLHCVDTRE 344
      381 MNKTNIRFMEPDS-----LFCVDPPE 401

RESULT 9
US-09-905-125A-69
; Sequence 69, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,638
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 69
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-69

Query Match      13.9%; Score 254; DB 4; Length 708;
Best Local Similarity 25.1%; Pred. No. 3.8e-15;
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

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      80 GPGYTT-----LAGDLSHNLTSISPTAFSRRLRYLESGLDSHNGLTALPASFPTS--SPL 133
      86 ---YSTDFPVNLGDLDSQNNLSVTINVKKMPQLLSVLEENKLTPEKCLSELNLT 142
      134 SDVNLSHNOJREVSVSAFTTHSGRALHYD-----LSNHLIR 171
      143 QELVYNHMLSTISPGAFGLHNLRLHNSNRLQMINSKFDPALPNEILMGENPILR 202
      172 L-----VHPPTAGLPAPTIQSLNLANRHLAVPNL---RDL 205
      203 IKMNMKPLINRLSVIAGINLIEIDNALVGL--ENLSISFYDNRLIKVHVALQKV 260
      206 PLRYSLDGNPLAVIGPGAFAGLGLTHLSLASLQRLPELAFSGFRELPGLOVLDLGNP 265
      261 NLKFLDLNKNPILNIRRGDFSNMLHKELGINNMPELISDLSLVNLPDLRKIEATNTP 320
      266 KLMWAGAEVSG:SSIOELDLSGTNLVPLPEALLHLPALQSVY-GQDVRCRLVR--- 321
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RESULT 10
US-09-902-775A-69
; Sequence 69, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

```

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 69  
LENGTH: 708  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-775A-69

Query Match 13.9%; Score 254; DB 4; Length 708;  
Best Local Similarity 25.1%; Pred. No. 3.8e-15;  
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

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DB 86 ---YSTDFPVNLGGLDISQNNLSSVTININVKMPQLISVYLENNKLTPEKLSLSNL 142  
QY 134 SDVNLISHNOLREVSVAFTTHSQGRALHVD-----LSHNLIR 171  
DB 143 QELIYNNHLLSTISPAFGILGHMLRLHNSNRLQMINSKFPALPMLTILMGENPIIR 202  
QY 172 L-----VPHPTAGPAPITQILNANRLHAVENL---RDL 205  
DB 203 IKDNNFKPLINRLSLVAGINLFEIPNNALVGL--ENLESISFYDKRLIVPVALQKV 260  
QY 206 PLYSLSDGNPLAVIGGAFAGLGLTHLSLASQLRLPELAPSGFRELPGQLVLDISGNP 265  
DB 261 NLKFLDINKPINKPINKIRGDDPSNMHLKELGINNMPELISDLSLVNLPPLRKITEATNP 320  
QY 266 KLNAGAEVPSGSLLELDLSTNVLVPEALILHPALQSVV--GQDYRCRLYR--- 321  
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QY 322 -EGTYPR--RPGSSPKVPLHCVDPR 344  
DB 381 MKNTINRMEPDS-----LFCVDPR 401

RESULT 11  
US-08-592-500-2  
Sequence 2, Application US/08592500  
Patent No. 6005089  
GENERAL INFORMATION:  
APPLICANT: Lanza, Francois  
APPLICANT: Phillips, David R.  
APPLICANT: Cazenave, Jean-Pierre  
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytcon Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentia Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,500  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,455  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 12418-28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-500-2

Query Match 13.5%; Score 247; DB 3; Length 560;  
Best Local Similarity 28.6%; Pred. No. 1.2e-14;  
Matches 112; Conservative 42; Mismatches 145; Indels 92; Gaps 14;

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Fri Aug 6 10:47:55 2004

us-10-017-390a-397.rapb

Page 1

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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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122	318.5	17.4	713	10	US-09-907-652-245	Sequence 245, App	195	267.5	14.6	673	10	US-09-990-662-52	Sequence 52, App
123	318.5	17.4	713	10	US-09-903-572A-245	Sequence 245, App	196	267.5	14.6	673	10	US-09-990-711-52	Sequence 52, App
124	318.5	17.4	713	10	US-09-902-979-245	Sequence 245, App	197	267.5	14.6	673	10	US-09-989-726-52	Sequence 52, App
125	318.5	17.4	713	10	US-09-905-125-245	Sequence 245, App	198	267.5	14.6	673	10	US-09-990-838-52	Sequence 52, App
126	318.5	17.4	713	10	US-09-906-815A-245	Sequence 245, App	199	267.5	14.6	673	10	US-09-998-156-52	Sequence 52, App
127	318.5	17.4	713	10	US-09-905-449-245	Sequence 245, App	200	267.5	14.6	673	10	US-09-990-737-52	Sequence 52, App
128	318.5	17.4	713	10	US-09-903-806-245	Sequence 245, App	201	267.5	14.6	673	10	US-09-991-157-52	Sequence 52, App
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132	318.5	17.4	713	10	US-09-903-603A-245	Sequence 245, App	205	267.5	14.6	673	10	US-09-990-726-52	Sequence 52, App
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146	318.5	17.4	713	12	US-09-904-485-245	Sequence 245, App	219	267.5	14.6	673	10	US-09-990-439-52	Sequence 52, App
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169	318.5	17.1	713	14	US-10-080-334-231	Sequence 231, App	242	267.5	14.6	673	10	US-09-989-662-52	Sequence 52, App
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238	267.5	14.6	673	12	US-10-063-512-16	Sequence 16, Appl	311	267.5	14.6	673	14	US-10-063-720-16	Sequence 16, Appl
239	267.5	14.6	673	12	US-10-063-513-16	Sequence 16, Appl	312	267.5	14.6	673	14	US-10-063-722-16	Sequence 16, Appl
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241	267.5	14.6	673	12	US-10-063-549-16	Sequence 16, Appl	314	267.5	14.6	673	14	US-10-063-728-16	Sequence 16, Appl
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248	267.5	14.6	673	12	US-10-063-553-16	Sequence 16, Appl	321	267.5	14.6	673	14	US-10-063-883-16	Sequence 16, Appl
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TIME OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT FILING DATE: US/09/946, 374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
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PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1828; DB 10; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5, 5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLAVSAGQTRPCPCQCEVEFTFGIFDSFSLTRYDCGGLGPHIMPVPIPIDT 60  
DB 1 MPWPLLLAVSAGQTRPCPCQCEVEFTFGIFDSFSLTRYDCGGLGPHIMPVPIPIDT 60  
QY AHIDSSNRLEWNEVSVALGPGYTTIAGLDLSHNLITISPTAFSRLRLTESLDLSHGL 120  
DB AHIDSSNRLEWNEVSVALGPGYTTIAGLDLSHNLITISPTAFSRLRLTESLDLSHGL 120  
QY 61 TALPASSTSPSLDVNLSHNOLREVSAFTTHSOGALHYDLSHNLHRLVPPPTAG 180  
DB 61 TALPASSTSPSLDVNLSHNOLREVSAFTTHSOGALHYDLSHNLHRLVPPPTAG 180  
QY 121 TALPASSTSPSLDVNLSHNOLREVSAFTTHSOGALHYDLSHNLHRLVPPPTAG 180  
DB 121 TALPASSTSPSLDVNLSHNOLREVSAFTTHSOGALHYDLSHNLHRLVPPPTAG 180  
QY 181 LPAFTQSILNLANRLLHVAVNLRLDLRLYLSIDGNFLAVIGGAFAGLGLTHLSLAIQ 240  
DB 181 LPAFTQSILNLANRLLHVAVNLRLDLRLYLSIDGNFLAVIGGAFAGLGLTHLSLAIQ 240  
QY 241 RLLELAPSGRELPGIOVLDSGNPKLNAGAEVSGLSLDELDSGTLNLPLEALL 300  
DB 241 RLLELAPSGRELPGIOVLDSGNPKLNAGAEVSGLSLDELDSGTLNLPLEALL 300  
QY 301 HLPALOSVSVGQDVRCLRLVREGTYPRRPGSSPKVYLHCVDTRRESAARGPTIL 353  
DB 301 HLPALOSVSVGQDVRCLRLVREGTYPRRPGSSPKVYLHCVDTRRESAARGPTIL 353

RESULT 2  
US-10-006-485A-397

Sequence 397, Application US/10006485A  
Publication No. US20030064062A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC9  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US/10/006,485A  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
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PRIOR FILING DATE: 1998-10-28

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Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEMPLLLIIVGCAQOTTRPCFCGCOCEVETFCULFSPSLTRVDCGLGHPVPIPIDT 60  
QY 61 AHDLSSNRLKEMVNESVILAGPGYTTLAGLDSHNLITSISPTAFSRRLRYESLDSHNGL 120  
DB 61 AHDLSSNRLKEMVNESVILAGPGYTTLAGLDSHNLITSISPTAFSRRLRYESLDSHNGL 120  
QY 121 TALPASFSTSSPLSDVNSHNLREVSVAFTTHSCGRALHYDLSHNLIRLVPHPTTAG 180  
DB 121 TALPASFSTSSPLSDVNSHNLREVSVAFTTHSCGRALHYDLSHNLIRLVPHPTTAG 180  
QY 181 LPAPTQSUNLAWNRHVAVPNLRDLPLRYSIDGNPLAVIGGAGAGLGLTHLSIASIQ 240  
DB 181 LPAPTQSUNLAWNRHVAVPNLRDLPLRYSIDGNPLAVIGGAGAGLGLTHLSIASIQ 240  
QY 241 RLEPLAPSGFRELPGIQLVDSGNPKLNWAGAEVFSGLSLOELDLSGTNLVPLDEALL 300  
DB 241 RLEPLAPSGFRELPGIQLVDSGNPKLNWAGAEVFSGLSLOELDLSGTNLVPLDEALL 300

QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 3

US-10-013-907A-397  
 / Sequence 397, Application US/10013907A  
 / Publication No. US20030064925A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan I.  
 / APPLICANT: Ferrera, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / FILE REFERENCE: F2830P1C34  
 / CURRENT APPLICATION NUMBER: US/10/013,907A  
 / PRIOR FILING DATE: 2001-12-10  
 / PRIOR APPLICATION removed - See File Wrapper or Palm  
 / NUMBER OF SEQ ID NOS: 477  
 / SEQ ID NO 397  
 / LENGTH: 353  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / US-10-013-907A-397

Query Match 100.0%; Score 1828; DB 12; Length 353;  
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 Db 1 MPMWLLLLAVSQAQTRPCPCPGCCQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 QY 61 AHLDLSNRLEWNEVSLAGPGYTTLAGLDLSHNLTSISPTAFSLRYLESLSLDSHNGL 120  
 Db 61 AHLDLSNRLEWNEVSLAGPGYTTLAGLDLSHNLTSISPTAFSLRYLESLSLDSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 Db 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 QY 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAFAGLGSLTHLSLSLQ 240  
 Db 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAFAGLGSLTHLSLSLQ 240  
 QY 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300  
 Db 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300  
 QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 4

US-10-015-499A-397  
 / Sequence 397, Application US/10015499A  
 / Publication No. US20030065142A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Pan, James  
 / APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan I.  
 / APPLICANT: Ferrera, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / FILE REFERENCE: F2830P1C42  
 / CURRENT APPLICATION NUMBER: US/10/015,499A  
 / PRIOR FILING DATE: 2001-12-11  
 / PRIOR APPLICATION removed - See File Wrapper or Palm  
 / NUMBER OF SEQ ID NOS: 477  
 / SEQ ID NO 397  
 / LENGTH: 353  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / US-10-015-499A-397

Query Match 100.0%; Score 1828; DB 12; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMWLLLLAVSQAQTRPCPCPGCCQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 Db 1 MPMWLLLLAVSQAQTRPCPCPGCCQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 QY 61 AHLDLSNRLEWNEVSLAGPGYTTLAGLDLSHNLTSISPTAFSLRYLESLSLDSHNGL 120  
 Db 61 AHLDLSNRLEWNEVSLAGPGYTTLAGLDLSHNLTSISPTAFSLRYLESLSLDSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 Db 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 QY 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAFAGLGSLTHLSLSLQ 240  
 Db 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAFAGLGSLTHLSLSLQ 240  
 QY 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300  
 Db 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300  
 QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 5

US-10-013-910A-397  
 / Sequence 397, Application US/10013910A  
 / Publication No. US20030187192A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan I.  
 / APPLICANT: Ferrera, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
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 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.

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/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2830PIC33
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/ PRIOR APPLICATION NUMBER: 60/099598
/ PRIOR FILING DATE: 1998-09-09
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 477
/ SEQ ID NO 397
/ LENGTH: 353
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-910A-397

Query Match          100.0%; Score 1828; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEWLLILLIAVSGAQTTRPCFPGCCQEVETFGFLPDSLSLTRVDCGGLGPHIMVPPIPDT 60
DB 1 MPEWLLILLIAVSGAQTTRPCFPGCCQEVETFGFLPDSLSLTRVDCGGLGPHIMVPPIPDT 60
QY 61 AHLDLSNRLEWNVESVLAGPGYTTLAGDLSHNLITISPTAFSRRLRYLESIDLSHNG 120
DB 61 AHLDLSNRLEWNVESVLAGPGYTTLAGDLSHNLITISPTAFSRRLRYLESIDLSHNG 120
QY 121 TALPAESFTSSPLSDVNLSHNQIREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQIREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
QY 181 LPAPTITSLNLAWRILAAVPLRDLPLRYLSIDGNPLAVTGGAGAGLGLTHLSIASIQ 240
DB 181 LPAPTITSLNLAWRILAAVPLRDLPLRYLSIDGNPLAVTGGAGAGLGLTHLSIASIQ 240
QY 241 RLPELAPSGFRRLPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
DB 241 RLPELAPSGFRRLPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
QY 301 HLPALQSVGVQDVRCLRRLVREGTTPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVGVQDVRCLRRLVREGTTPRRPGSSPKVPLHCVDTRESAARGPTIL 353

RESULT 6
US-10-226-254A-397
/ Sequence 397, Application US/10226254A
/ Publication No. US20030224478A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Deanoys, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
```

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/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2830PIC68
/ CURRENT FILING DATE: 2002-08-21
/ PRIOR APPLICATION NUMBER: 60/098716
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: 60/098723
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: 60/098749
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: 60/098750
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: 60/098803
/ PRIOR FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: 60/098821
/ PRIOR FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: 60/098843
/ PRIOR FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: 60/099536
/ PRIOR FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: 60/099596
/ PRIOR FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: 60/099598
/ PRIOR FILING DATE: 1998-09-09
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 477
/ SEQ ID NO 397
/ LENGTH: 353
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-226-254A-397

Query Match          100.0%; Score 1828; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEWLLILLIAVSGAQTTRPCFPGCCQEVETFGFLPDSLSLTRVDCGGLGPHIMVPPIPDT 60
DB 1 MPEWLLILLIAVSGAQTTRPCFPGCCQEVETFGFLPDSLSLTRVDCGGLGPHIMVPPIPDT 60
QY 61 AHLDLSNRLEWNVESVLAGPGYTTLAGDLSHNLITISPTAFSRRLRYLESIDLSHNG 120
DB 61 AHLDLSNRLEWNVESVLAGPGYTTLAGDLSHNLITISPTAFSRRLRYLESIDLSHNG 120
QY 121 TALPAESFTSSPLSDVNLSHNQIREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQIREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
QY 181 LPAPTITSLNLAWRILAAVPLRDLPLRYLSIDGNPLAVTGGAGAGLGLTHLSIASIQ 240
DB 181 LPAPTITSLNLAWRILAAVPLRDLPLRYLSIDGNPLAVTGGAGAGLGLTHLSIASIQ 240
QY 241 RLPELAPSGFRRLPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
DB 241 RLPELAPSGFRRLPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
QY 301 HLPALQSVGVQDVRCLRRLVREGTTPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVGVQDVRCLRRLVREGTTPRRPGSSPKVPLHCVDTRESAARGPTIL 353

RESULT 7
US-10-015-395A-397
/ Sequence 397, Application US/10015395A
```

Publication No. US20040073015A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830P1C57  
CURRENT APPLICATION NUMBER: US/10/015,395A  
CURRENT FILING DATE: 2001-12-12  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
LENGTH: 353  
SEQ ID NO 397  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-395A-397

Query Match 100.0%; Score 1828; DB 12; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5,5e-156; Indels 0; Gaps 0;  
Matches 353; Conservative 0; Mismatches 0;

QY 1 MPWPLLLLVASGQTRPCPCGCCVEFTFGFDSFSLTRVDCSGLGHIMPVPIPLDT 60  
DB 1 MPWPLLLLVASGQTRPCPCGCCVEFTFGFDSFSLTRVDCSGLGHIMPVPIPLDT 60  
QY 61 AHLDSSNRLEWNEVSVAAGPGYTTLAGDLSHNLITSISPTAFSRLRYLESIDLSHNGI 120  
DB 61 AHLDSSNRLEWNEVSVAAGPGYTTLAGDLSHNLITSISPTAFSRLRYLESIDLSHNGI 120  
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGCRALHVDLSHNLIRLVPHPTTAG 180  
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGCRALHVDLSHNLIRLVPHPTTAG 180  
QY 181 LPAPTIQSILNANRLHVAENVLDLPLRYLSLDGNPLAVIGGAFAGLGLTHLSIASIQ 240  
DB 181 LPAPTIQSILNANRLHVAENVLDLPLRYLSLDGNPLAVIGGAFAGLGLTHLSIASIQ 240  
QY 241 RLPELAPSGRELPGIQLVDLSGNPKLNWAGAVFSGLSLDELDSGTLVLPBALLL 300  
DB 241 RLPELAPSGRELPGIQLVDLSGNPKLNWAGAVFSGLSLDELDSGTLVLPBALLL 300  
QY 301 HLPALQSVSVGQDVRCLRVRBGTYPRRPSSPKVPLHCVDTRESAARGPTIL 353  
DB 301 HLPALQSVSVGQDVRCLRVRBGTYPRRPSSPKVPLHCVDTRESAARGPTIL 353

RESULT 8  
US-10-006-856A-397  
Sequence 397, Application US/10006856A  
Publication No. US20030044841A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830P1C14  
CURRENT APPLICATION NUMBER: US/10/006,856A  
CURRENT FILING DATE: 2002-05-10  
NUMBER OF SEQ ID NOS: 477  
Prior Application removed - See file Wrapper or Palm  
SEQ ID NO 397  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-006-856A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5,5e-156; Indels 0; Gaps 0;  
Matches 353; Conservative 0; Mismatches 0;

QY 1 MPWPLLLLVASGQTRPCPCGCCVEFTFGFDSFSLTRVDCSGLGHIMPVPIPLDT 60  
DB 1 MPWPLLLLVASGQTRPCPCGCCVEFTFGFDSFSLTRVDCSGLGHIMPVPIPLDT 60  
QY 61 AHLDSSNRLEWNEVSVAAGPGYTTLAGDLSHNLITSISPTAFSRLRYLESIDLSHNGI 120  
DB 61 AHLDSSNRLEWNEVSVAAGPGYTTLAGDLSHNLITSISPTAFSRLRYLESIDLSHNGI 120  
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGCRALHVDLSHNLIRLVPHPTTAG 180  
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGCRALHVDLSHNLIRLVPHPTTAG 180  
QY 181 LPAPTIQSILNANRLHVAENVLDLPLRYLSLDGNPLAVIGGAFAGLGLTHLSIASIQ 240  
DB 181 LPAPTIQSILNANRLHVAENVLDLPLRYLSLDGNPLAVIGGAFAGLGLTHLSIASIQ 240  
QY 241 RLPELAPSGRELPGIQLVDLSGNPKLNWAGAVFSGLSLDELDSGTLVLPBALLL 300  
DB 241 RLPELAPSGRELPGIQLVDLSGNPKLNWAGAVFSGLSLDELDSGTLVLPBALLL 300  
QY 301 HLPALQSVSVGQDVRCLRVRBGTYPRRPSSPKVPLHCVDTRESAARGPTIL 353  
DB 301 HLPALQSVSVGQDVRCLRVRBGTYPRRPSSPKVPLHCVDTRESAARGPTIL 353

RESULT 9  
US-10-006-818A-397  
Sequence 397, Application US/10006818A  
Publication No. US20030054406A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830P1C4  
CURRENT APPLICATION NUMBER: US/10/006,818A  
CURRENT FILING DATE: 2001-12-06  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 397



LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-006-818A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60  
DB 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60  
QY 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
DB 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
QY 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
DB 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
QY 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240  
DB 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240  
QY 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWMAEVSGLSLOELDLSGTNLVPLPEALL 300  
DB 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWMAEVSGLSLOELDLSGTNLVPLPEALL 300  
QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353  
DB 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

## RESULT 10

US-10-015-393A-397  
Sequence 397, Application US/10015393A  
Publication No. US20030069179A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830PIC46  
CURRENT APPLICATION NUMBER: US/10/015.393A  
CURRENT FILING DATE: 2002-06-10  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 397  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-393A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60  
DB 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60

QY 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
DB 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
QY 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
DB 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
QY 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240  
DB 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240  
QY 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWMAEVSGLSLOELDLSGTNLVPLPEALL 300  
DB 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWMAEVSGLSLOELDLSGTNLVPLPEALL 300  
QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353  
DB 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

## RESULT 11

US-10-015-869A-397  
Sequence 397, Application US/10015869A  
Publication No. US20030073130A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830PIC45  
CURRENT APPLICATION NUMBER: US/10/015.869A  
CURRENT FILING DATE: 2002-06-25  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 397  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-869A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60  
DB 1 MWPULLLLAVSQAQTRPCFPGCCQCEVETFGLPFSFSLTRVDCSGLGPHIMVPPIPDT 60  
QY 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
DB 61 AHDLSNRLEWNEVSILAGPGYTTLAGLDSHNLITSIPAFSLRYLESIDLSHNGL 120  
QY 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
DB 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180  
QY 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240  
DB 181 LPAPTIOGLNLAWRHLAVENLRDLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLSAQ 240

QY 241 RLEPLAPSGFREIPGQVLDLSGNPKLNAGAEVFSGLSLOELDLSGNNVLPBEALL 300  
DB 241 RLEPLAPSGFREIPGQVLDLSGNPKLNAGAEVFSGLSLOELDLSGNNVLPBEALL 300  
QY 301 HLPALQSVGVQDVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTTL 353  
DB 301 HLPALQSVGVQDVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTTL 353

RESULT 12  
US-10-012-121A-397  
; Sequence 397, Application US/10012121A  
; Publication No.: US20030073810A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C20  
CURRENT APPLICATION NUMBER: US/10/012,121A  
CURRENT FILING DATE: 2001-12-07  
Prior Application removed - See File Wrapper or Palm  
SEQU ID NO 397  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-012-121A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLAVSGAQTTRPCPGCCQCEVEFTFGLFDSFLTRVDCSGLGPHIMVPPIPLDT 60  
DB 1 MPWPLLLAVSGAQTTRPCPGCCQCEVEFTFGLFDSFLTRVDCSGLGPHIMVPPIPLDT 60  
QY 61 AHLDLSNRLNEMNEBVLGPGYTTLAGLDLSHNLTSISPTAFSRLYLSLDSHNGL 120  
DB 61 AHLDLSNRLNEMNEBVLGPGYTTLAGLDLSHNLTSISPTAFSRLYLSLDSHNGL 120  
QY 121 TALPASFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLTHRLVPHPTAG 180  
DB 121 TALPASFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLTHRLVPHPTAG 180  
QY 181 LEPMTIOSLNNRRHAYPNLFDLPRLTSLDGNLAVYTGAPAPGGLGTHLSIASIQ 240  
DB 181 LEPMTIOSLNNRRHAYPNLFDLPRLTSLDGNLAVYTGAPAPGGLGTHLSIASIQ 240  
QY 241 RLEPLAPSGFREIPGQVLDLSGNPKLNAGAEVFSGLSLOELDLSGNNVLPBEALL 300  
DB 241 RLEPLAPSGFREIPGQVLDLSGNPKLNAGAEVFSGLSLOELDLSGNNVLPBEALL 300  
QY 301 HLPALQSVGVQDVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTTL 353  
DB 301 HLPALQSVGVQDVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTTL 353

RESULT 13  
US-10-006-116A-397

Sequence 397, Application US/10006116A  
Publication No.: US20030082626A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C15  
CURRENT APPLICATION NUMBER: US/10/006,116A  
CURRENT FILING DATE: 2001-12-16  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661

Fri Aug 6 10:47:55 2004

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Page 13

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DB 61 AHDLSNRLEVNNSVLAGPGYTLGLDLSHNLTSISPTAFRLRYLESLSHGL 120  
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DB 121 TALPASFSSPLSDVNSHNLREVSVAPFTTHSQGRALHVDLSHNLHRLVPHPTBAG 180  
QY 181 LPAPTQSLNANRRLHAVENRDLPLRYLSLDSNPPLAVTGGAGAGGLTHLSLASIQ 240  
DB 181 LPAPTQSLNANRRLHAVENRDLPLRYLSLDSNPPLAVTGGAGAGGLTHLSLASIQ 240

Db 181 LPAPTQSLNLANRRLHAVNRLDLPRLYSLDGNPLAVIGPAGAG:GGLTHLSASLQ 240  
Qy 241 RUPELAPSGFREIPGQVLDLSGNPKLNAGAEVSGSLSDLELDLSGNLVPLPEALL 300  
Db 241 RUPELAPSGFREIPGQVLDLSGNPKLNAGAEVSGSLSDLELDLSGNLVPLPEALL 300  
Qy 301 HUPALQSVGVGDVRCRLVREGTYPRRPGSSPKVPLHCVDTRRESAARGPTIL 353  
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; Sequence 397, Application US/10006117A  
; Publication No. US20030082627A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan 1.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C13  
; CURRENT APPLICATION NUMBER: US/10/006,117A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 477  
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; ORGANISM: Homo sapiens  
US-10-006-117A-397

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Db 61 AHDLSNRLNEMNESVLAGPGYTTLAGLDLSHNLITS:SPTRFSLRLYLSLDSHNGL 120  
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; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan 1.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C13  
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61 AHLDLSSNRLEMYNSVLGAPGYTTIAGLDLSHNLLTISPTAFSRLRYLESIDLSHNGL 120
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121 TALPASFTSSPLSDVNLGNQLREYVSVAFTTHSQGRALHVDLSHNLTHRLVLPHPETRAG 180
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121 TALPASFTSSPLSDVNLGNQLREYVSVAFTTHSQGRALHVDLSHNLTHRLVLPHPETRAG 180
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Fri Aug 6 10:47:55 2004

Qy	181	LPAPTIOSLNLAWNRIHVPNIRDLPLRYLSLDGNPLAVIGGAFAGLGGTHLSLASLQ	240
Db	181	LPAPTIOSLNLAWNRIHVPNIRDLPLRYLSLDGNPLAVIGGAFAGLGGTHLSLASLQ	240
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Db	241	RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFGSLSSLOELDLSCGTNLVPLPEALLL	300
Qy	301	HLPALQSVSVGQDVRRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL	353
Db	301	HLPALQSVSVGQDVRRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL	353

Search completed: August 2, 2004, 16:27:27  
Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2004, 16:04:02 ; Search time 13 Seconds

(without alignments)  
1413.905 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1826

Sequence: 1 MPWPLLLLLAVSGAQTTPC.....KVPLHCVDRBSAARGPTIL 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	313.5	17.1	713	1	GARP_HUMAN
2	279.5	15.3	662	1	Q14392 homo sapien
3	265	14.5	907	1	LGR5_MOUSE
4	257	14.1	907	1	Q921P4 homo sapien
5	257	14.1	951	1	LGR4_HUMAN
6	256	14.0	951	1	LGR4_RAT
7	248	13.6	347	1	A2GL_HUMAN
8	247	13.5	560	1	GPV_HUMAN
9	240	13.1	578	1	LR15_RAT
10	239.5	13.1	567	1	GPV_RAT
11	238.5	13.0	379	1	ASPN_HUMAN
12	238	13.0	905	1	TLR3_MOUSE
13	234.5	12.8	605	1	ALS_PAPHA
14	232	12.7	373	1	ASPN_MOUSE
15	227	12.4	581	1	LR15_HUMAN
16	224.5	12.3	605	1	ALS_HUMAN
17	224	12.3	1529	1	SLR2_HUMAN
18	221.5	12.1	828	1	LGR6_HUMAN
19	220.5	12.1	782	1	CHAO_TRICA
20	220.5	12.1	904	1	TLR3_HUMAN
21	218.5	12.0	1032	1	TLR9_HUMAN
22	218	11.9	567	1	GPV_MOUSE
23	215.5	11.8	603	1	ALS_RAT
24	214.5	11.7	603	1	ALS_MOUSE
25	212	11.6	357	1	PGS2_CHICK
26	211.5	11.6	1256	1	FLII_DROME
27	209	11.4	356	1	PGS2_COTJA
28	207.5	11.4	733	1	CT75_MOUSE
29	205.5	11.2	481	1	NYX_HUMAN
30	204	11.2	582	1	SHO2_MOUSE
31	203	11.1	582	1	SHO2_HUMAN
32	199	10.9	338	1	LUM_HUMAN
33	198.5	10.9	360	1	PGS2_PIG

34	198.5	10.9	473	1	RT4R_HUMAN
35	198	10.8	354	1	PGS2_RAT
36	197	10.8	476	1	NYX_MOUSE
37	197	10.8	536	1	CBP8_HUMAN
38	197	10.8	1315	1	CHAO_DROME
39	196.5	10.7	360	1	PGS2_SHEEP
40	195.5	10.7	360	1	PGS2_BOVIN
41	195.5	10.7	360	1	PGS2_RABIT
42	195.5	10.7	740	1	CT75_HUMAN
43	194.5	10.6	354	1	PGS2_MOUSE
44	194	10.6	858	1	TLR5_HUMAN
45	193.5	10.6	342	1	LUM_BOVIN
46	192.5	10.5	360	1	PGS2_HORSE
47	191.5	10.5	1024	1	POPC_RALSO
48	191	10.4	1504	1	SLIT_DROME
49	190.5	10.4	359	1	PGS2_HUMAN
50	190.5	10.4	473	1	RT4R_MACFA
51	190.5	10.4	1032	1	TLR9_MOUSE
52	188.5	10.3	338	1	LUM_MOUSE
53	188.5	10.3	369	1	PGS1_BOVIN
54	187	10.2	360	1	PGS2_CANFA
55	187	10.2	372	1	PGS1_HORSE
56	186	10.2	754	1	LGR8_HUMAN
57	185.5	10.1	343	1	LUM_COTJA
58	184.5	10.1	331	1	PLIE_AKBL
59	183.5	10.0	338	1	LUM_RAT
60	183.5	10.0	369	1	PGS1_MOUSE
61	183.5	10.0	369	1	PGS1_RAT
62	182.5	10.0	369	1	PGS1_CANFA
63	182.5	10.0	369	1	PGS1_SHEEP
64	181.5	9.9	343	1	LUM_CHICK
65	181	9.9	496	1	TMW_ARATH
66	181	9.9	859	1	TLR5_MOUSE
67	180.5	9.9	440	1	OMGP_MOUSE
68	180	9.8	368	1	PGS1_HUMAN
69	180	9.8	1269	1	FLIH_HUMAN
70	179.5	9.8	440	1	OMGP_HUMAN
71	179.5	9.8	473	1	RT4R_MOUSE
72	179	9.8	1039	1	YR71_CABEL
73	177.5	9.7	368	1	PGS1_XENIA
74	177.5	9.7	649	1	FLR3_HUMAN
75	176	9.6	376	1	FMOD_RAT
76	176	9.6	1257	1	FLIH_CABEL
77	175	9.6	378	1	PRLP_MOUSE
78	175	9.6	473	1	RT4R_RAT
79	173.5	9.5	1032	1	TLR8_MOUSE
80	172	9.4	361	1	CHAD_BOVIN
81	172	9.4	376	1	FMOD_MOUSE
82	171.5	9.4	626	1	GPBA_HUMAN
83	171.5	9.4	682	1	CONN_DROME
84	171	9.4	375	1	FMOD_BOVIN
85	171	9.4	376	1	FMOD_HUMAN
86	170	9.3	358	1	CHAD_RAT
87	169	9.2	358	1	CHAD_MOUSE
88	167	9.1	423	1	OMD_RAT
89	167	9.1	851	1	NUDI_YEAST
90	165.5	9.1	359	1	CHAD_HUMAN
91	165.5	9.1	1115	1	GPCR_LYMTST
92	165	9.0	2493	1	CYAA_USTMA
93	164.5	9.0	757	1	LGR7_HUMAN
94	164.5	9.0	2300	1	CYAA_NEUCR
95	163	8.9	699	1	ECM2_HUMAN
96	163	8.9	737	1	LGR8_MOUSE
97	163	8.9	1839	1	CYAA_SACKL
98	162.5	8.9	646	1	FLR1_HUMAN
99	162	8.9	377	1	PRLP_RAT
100	162	8.9	2026	1	CYAA_YEAST
101	161	8.8	1041	1	TLR8_HUMAN
102	160	8.8	839	1	TLR4_HUMAN
103	159.5	8.7	192	1	LUM_RABIT
104	159	8.7	382	1	PRLP_HUMAN
105	159	8.7	839	1	TLR4_PANPA
106	158	8.6	1097	1	TOLL_DROME

Q9bzt6	homo sapien
Q01129	rattus norv
P43503	mus musculus
P22792	homo sapien
P12024	drosophila
Q9tt62	ovis aries
P21793	bos taurus
Q8wt88	oryctolagus
Q28848	homo sapien
P28654	mus musculus
O60602	homo sapien
Q05443	bos taurus
Q46542	equus caball
Q9r822	raistonia s
P24014	drosophila
P07585	homo sapien
Q3n0a3	macaca fasc
Q9equ3	mus musculus
P51885	mus musculus
P21809	bos taurus
Q29333	canis fami
Q46403	equus caball
Q8wx40	homo sapien
Q9de77	coturnix co
Q93233	agkistrodon
P51886	rattus norv
P28653	mus musculus
P47853	rattus norv
Q02678	canis fami
Q46390	ovis aries
P51890	gallus gall
Q38641	arabidopsis
Q9j1f7	mus musculus
Q63912	mus musculus
P21810	homo sapien
Q13045	homo sapien
P23515	homo sapien
Q99pi8	mus musculus
Q09564	caenorhabdi
Q9ib75	xenopus lae
P50609	homo sapien
P34268	caenorhabdi
Q9jk53	mus musculus
Q99m75	rattus norv
P58692	mus musculus
Q27972	bos taurus
P50608	mus musculus
P07359	homo sapien
Q01819	drosophila
P13605	bos taurus
Q06828	homo sapien
O70210	rattus norv
Q55246	mus musculus
Q92167	rattus norv
P32336	saccharomyc
Q15335	homo sapien
P46023	lymaea sta
P49606	utillago ma
Q9bbx9	homo sapien
Q01631	neurospora
Q94769	homo sapien
Q91225	mus musculus
P23466	saccharomyc
Q9nzu1	homo sapien
Q9eqp5	rattus norv
P08678	saccharomyc
Q9nr57	homo sapien
O00206	homo sapien
Q46379	oryctolagus
P51888	homo sapien
Q9ttt0	pan paniscu
P08953	drosophila

107	158	8.6	1192	1	EXS ARATH	Q9lyn8 arabidopsis	180	126	6.9	299	1	MIME_BOVIN	P19879 bos taurus
108	157.5	8.6	257	1	LR3 MOUSE	P59034 mus musculus	181	125.5	6.9	373	1	CD14_BOVIN	Q95122 bos taurus
109	157.5	8.6	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien	182	125.5	6.9	687	1	FSHR_EQUAS	Q95179 equus asinu
110	157	8.6	272	1	PGS1_PIG	Q9gkq6 sus scrofa	183	125.5	6.9	810	1	LR8C_HUMAN	Q81wt6 homo sapien
111	157	8.6	623	1	PALP_HUMAN	Q9qtb4 homo sapien	184	125.5	6.9	925	1	SLDR_ANGEL	P35409 anthopleura
112	157	8.6	661	1	C180_MOUSE	Q92192 mus musculus	185	124.5	6.8	338	1	SD22_YEAST	P36047 saccharomyc
113	157	8.6	833	1	TLR4_FELCA	P58727 felis silve	186	124.5	6.8	910	1	LR8C_MOUSE	Q80wg5 mus musculus
114	155.5	8.5	380	1	FMOD_CHICK	P51887 gallus gall	187	123	6.7	784	1	TLR2_CRIGR	Q9rlf8 cricetus
115	155.5	8.5	843	1	TLR4_HORSE	Q9myw3 equus cabal	188	122.5	6.7	257	1	LRK3_HUMAN	Q9by71 homo sapien
116	155	8.5	1207	1	BR11_LYCPPE	Q81899 lycopersico	189	122.5	6.7	784	1	TLR2_MOUSE	Q9qun7 mus musculus
117	154	8.4	381	1	PRLP_BOVIN	Q8qkn8 bos taurus	190	122	6.7	795	1	TLR2_MOUSE	P33543 arabidopsis
118	154	8.4	1207	1	BR11_LYCES	Q8qun5 lycopersico	191	121.5	6.6	674	1	TLR1_ARATH	Q920a0 mus musculus
119	152.5	8.3	257	1	LR3 RAT	P59035 rattus norv	192	121	6.6	328	1	OPT_MOUSE	K8k1s1 mus musculus
120	152	8.3	841	1	TLR4_BOVIN	Q9g165 bos taurus	193	121	6.6	537	1	IG14_MOUSE	P23799 trypanosoma
121	151.5	8.3	423	1	OMD_MOUSE	Q35103 mus musculus	194	120.5	6.6	630	1	ESR8_HYBB	P47799 equus cabal
122	151.5	8.3	826	1	TLR4_PAPAN	Q9tsp2 papio anubi	195	120	6.6	694	1	FSHR_HORSE	Q63691 rattus norv
123	150.5	8.2	977	1	Y848_HUMAN	Q94933 homo sapien	196	119	6.5	371	1	CD14_RAT	Q9dd78 gallus gall
124	150.5	8.2	1050	1	TLR7_MOUSE	P58681 mus musculus	197	118	6.5	793	1	TL21_CHICK	Q951a9 bos taurus
125	150	8.2	326	1	YN29_CABEL	P45969 caenorhabdi	198	117.5	6.4	784	1	TLR2_BOVIN	P14770 homo sapien
126	148.5	8.1	793	1	CD11_HUMAN	Q9y219 homo sapien	199	116.5	6.4	177	1	GP1X_HUMAN	Q9m519 arabidopsis
127	148	8.1	835	1	TLR4_MOUSE	Q9qk6 mus musculus	200	116	6.3	330	1	YDDK_ECOLI	P76123 escherichia
128	148	8.1	966	1	Y918_HUMAN	Q94991 homo sapien	201	115.5	6.3	318	1	FSHR_SHEEP	P35379 ovis aries
129	147	8.0	351	1	KERA_MOUSE	Q35367 mus musculus	202	115.5	6.3	695	1	YDDK_ECOLI	P43298 arabidopsis
130	147	8.0	800	1	INLA_LISMO	P25146 listeria mo	203	115.5	6.3	942	1	TMK1_ARATH	P10810 mus musculus
131	145	7.9	838	1	TLR4_CRIGR	Q9v82 cricetus	204	114	6.2	366	1	CD14_MOUSE	P12259 homo sapien
132	145	7.9	1196	1	BR11_ARATH	O22476 arabidopsis	205	114	6.2	224	1	PA5_HUMAN	P55456 rhizobium s
133	145	7.9	327	1	OPT_CANFA	P83286 canis famli	206	113.5	6.2	756	1	Y4FR_RHIN	Q8vab8 mus musculus
134	144.5	7.9	375	1	CD14_HUMAN	P85571 homo sapien	207	113.5	6.2	795	1	TLR1_MOUSE	Q9epq1 mus musculus
135	144.5	7.9	298	1	MIME_MOUSE	Q62000 mus musculus	208	113	6.2	518	1	LR2_MOUSE	Q8vab8 mus musculus
136	143	7.8	332	1	OPT_HUMAN	Q9ubm4 homo sapien	209	113	6.2	632	1	PAC2_YEAST	P39337 saccharomyc
137	142.5	7.8	147	1	FMOD_RABIT	O46378 cryotolagus	210	112.5	6.2	330	1	PG12_ARATH	Q9m518 arabidopsis
138	142.5	7.8	294	1	MIME_CHICK	Q9w6ho gallus gall	211	112.5	6.2	630	1	ESR8_TYEO	P26337 trypanosoma
139	142.5	7.8	2145	1	CYAA_PODAN	Q91513 podopora a	212	112.5	6.2	796	1	TLR8_HUMAN	Q9y2c9 homo sapien
140	142	7.8	352	1	KERA_BOVIN	O62702 bos taurus	213	112	6.1	825	1	TRK2_PIG	P24786 sus scrofa
141	142	7.8	1692	1	CYAA_SCHPO	P14605 schizosacch	214	111.5	6.1	839	1	TRK2_HUMAN	Q16288 homo sapien
142	141.5	7.7	293	1	MIME_COTJA	Q9de65 coturnix co	215	111	6.1	839	1	FSHR_BOVIN	P35376 bos taurus
143	141.5	7.7	321	1	PG1B_BOVIN	P79119 bos taurus	216	110.5	6.0	695	1	YQOA_CABEL	Q09299 caenorhabdi
144	141.5	7.7	617	1	PALP_RAT	Q9jmh2 rattus norv	217	110	6.0	699	1	PGCA_BOVIN	P13608 bos taurus
145	141	7.7	322	1	PG1B_HUMAN	Q9jmh2 rattus norv	218	109.5	6.0	2364	1	TSHR_CANFA	P14763 canis famli
146	140.5	7.7	322	1	LUM_PIG	Q9tcb4 sus scrofa	219	109	6.0	764	1	CLV1_ARATH	Q9syg8 arabidopsis
147	140.5	7.7	353	1	KERA_CHICK	O42235 gallus gall	220	109	6.0	980	1	FSHR_MOUSE	P35378 mus musculus
148	140.5	7.7	353	1	KERA_COTJA	Q9de66 coturnix co	221	108.5	5.9	632	1	TRK2_RAT	Q63604 rattus norv
149	140.5	7.7	781	1	TL22_CHICK	Q9dgb6 gallus gall	222	108.5	5.9	821	1	TRK2_RAT	Q91r4 arabidopsis
150	140.5	7.7	618	1	PALP_MOUSE	Q8k099 mus musculus	223	108.5	5.9	1054	1	R131_ARATH	P47750 mus musculus
151	139.5	7.6	414	1	LLR1_HUMAN	Q96150 homo sapien	224	108	5.9	764	1	TSHR_MOUSE	Q9by88 homo sapien
152	138.5	7.6	421	1	OMD_HUMAN	Q99983 homo sapien	225	107.5	5.9	371	1	LR2_HUMAN	Q15399 homo sapien
153	138	7.5	322	1	PG1B_MOUSE	P70186 mus musculus	226	107	5.9	2944	1	TLR1_HUMAN	Q15399 homo sapien
154	137	7.5	409	1	YOPM_YERPE	P17778 yersinia pe	227	106.5	5.8	786	1	SD22_SCHPO	P22194 schizosacch
155	136	7.4	352	1	KERA_HUMAN	O60938 homo sapien	228	105	5.7	332	1	FSHR_MACFA	P22194 macaca fasc
156	136	7.4	999	1	RLK5_ARATH	P47735 arabidopsis	229	105	5.7	695	1	FSHR_MOUSE	P22194 macaca fasc
157	135.5	7.4	342	1	PG13_PHAVU	P58823 phaseolus v	230	104.5	5.7	764	1	TRK2_RAT	P22194 macaca fasc
158	135.5	7.4	537	1	LG14_HUMAN	Q8n135 homo sapien	231	104.5	5.7	864	1	TRK2_RAT	P22194 macaca fasc
159	135	7.4	316	1	PG1B_CHICK	Q90944 gallus gall	232	104	5.7	526	1	MITF_MOUSE	Q08874 mus musculus
160	135	7.4	372	1	D100_ARATH	Q00874 arabidopsis	233	104	5.7	695	1	FSHR_HUMAN	Q9by88 homo sapien
161	134	7.3	4303	1	PKD1_HUMAN	P98161 homo sapien	234	103.5	5.7	330	1	PGIP_PYRGO	Q05091 pyrus commu
162	133	7.3	784	1	TLR2_MACFA	Q95m53 macaca fasc	235	103.5	5.7	538	1	LSHR_SHEEP	Q28585 ovis aries
163	132	7.2	422	1	OMD_BOVIN	O77742 bos taurus	236	103.5	5.7	763	1	TSHR_BOVIN	Q27987 bos taurus
164	131.5	7.2	835	1	TLR1_RAT	Q9qx05 rattus norv	237	103	5.6	521	1	NOR2_ALCEU	Q9k4u8 alcaligenes
165	131.5	7.2	1021	1	PSR2_DAUCA	Q81pb4 daucus caro	238	103	5.6	526	1	MITF_HUMAN	Q75030 homo sapien
166	131	7.2	548	1	LG13_MOUSE	Q8k406 mus musculus	239	102.5	5.6	615	1	BAK1_ARATH	Q94f62 arabidopsis
167	130.5	7.1	276	1	RSU1_HUMAN	Q15404 homo sapien	240	102	5.6	695	1	FSHR_PIG	P49059 sus scrofa
168	130	7.1	372	1	CD14_RABIT	P28680 cryotolagus	241	102	5.6	235	1	ZEAC_MAIZE	P24449 zea mays (m
169	129.5	7.1	342	1	PG11_PHAVU	P35334 phaseolus v	242	102	5.6	774	1	ENFC_PSEAE	Q9hyb8 pseudomonas
170	129	7.1	276	1	RSU1_MOUSE	Q01730 mus musculus	243	101.5	5.6	259	1	LP15_MOUSE	Q96pb8 homo sapien
171	129	7.1	661	1	C180_HUMAN	Q99467 homo sapien	244	101.5	5.6	259	1	TRK2_CHICK	Q96pb8 homo sapien
172	129	7.1	784	1	TLR2_HUMAN	O60603 homo sapien	245	100	5.5	135	1	PGS1_RABIT	Q91044 gallus gall
173	128.5	7.0	574	1	IPM4_SHIFL	P18009 shigella fl	246	100	5.5	827	1	TRK2_CHICK	Q46377 cryotolagus
174	128.5	7.0	660	1	FLR2_HUMAN	O43155 homo sapien	247	100	5.5	811	1	TLR4_HUMAN	Q96bx5 homo sapien
175	127.5	7.0	548	1	LG13_HUMAN	Q8n145 homo sapien	248	99.5	5.4	493	1	Y014_HUMAN	Q15048 homo sapien
176	127	6.9	298	1	MIME_HUMAN	P20774 homo sapien	249	99.5	5.4	778	1	TRKA_CHICK	Q91009 gallus gall
177	127	6.9	1008	1	PSKR_ARATH	Q9zv77 arabidopsis	250	99.5	5.4	956	1	PMAB_ARATH	Q91v11 arabidopsis
178	126.5	6.9	342	1	PG12_PHAVU	P58822 phaseolus v	251	99	5.4	1447	1	BIRB_MOUSE	Q9guk4 mus musculus
179	126.5	6.9	545	1	LG12_HUMAN	Q8n0v4 homo sapien	252	98	5.4	557	1	LG11_HUMAN	Q95970 homo sapien



253	98	5.4	557	1	LG11 MOUSE	Q9jial mus musculus	326	88.5	4.8	234	1	ZEAL MAIZE	P02859 zea mays (m
254	98	5.4	557	1	LG11 RAT	Q9k4y5 rattus norv	327	88.5	4.8	338	1	PO43 HUMAN	Q15319 homo sapien
255	98	5.4	764	1	TSRB SHREP	P56495 ovis aries	328	88.5	4.8	386	1	RNA1 SCHPO	P41391 schizosacch
256	98	5.4	821	1	TRKB MOUSE	P15209 mus musculus	329	88.5	4.8	855	1	MUTS_PSEAE	Q9hy08 pseudomonas
257	97.5	5.3	773	1	YOD3 CAEEL	P34595 caenorhabdi	330	88	4.8	206	1	GPBB HUMAN	P13224 homo sapien
258	97	5.3	456	1	RINI_PIG	P79763 sus scrofa	331	88	4.8	928	1	BCS3 HUMAN	Q9h6u6 homo sapien
259	97	5.3	693	1	FHR CHICK	P19775 gallus gall	332	88	4.8	957	1	PMAL_NICPL	Q08435 nicotiana p
260	97	5.3	701	1	LSHR BOVIN	Q28005 bos taurus	333	88	4.8	1114	1	RET HUMAN	P07949 homo sapien
261	97	5.3	764	1	TSRH HUMAN	P16473 homo sapien	334	88	4.8	1115	1	FRPA_NEIMC	P55126 neisseria m
262	97	5.3	928	1	BCS3 MOUSE	Q8ccn5 mus musculus	335	88	4.8	1829	1	FRPC_NEIMC	P55127 neisseria m
263	96.5	5.3	532	1	IP47 SHIFL	P18014 shigella fl	336	88	4.8	2167	1	SHK1 RAT	Q9wv48 rattus norv
264	96.5	5.3	794	1	TRK1 LYMT	O76997 lymphaea sta	337	88	4.8	2415	1	PGCA HUMAN	P16112 homo sapien
265	96	5.3	263	1	ZEAX MAIZE	P04700 zea mays (m	338	88	4.8	2936	1	NBEA MOUSE	Q9epn1 mus musculus
266	96	5.3	266	1	ZEAX MAIZE	P04699 zea mays (m	339	87.5	4.8	234	1	ZEAX MAIZE	P06675 zea mays (m
267	96	5.3	1258	1	GLI2 HUMAN	P10070 homo sapien	340	87.5	4.8	466	1	VL2 HPV52	P36763 human papil
268	95.5	5.2	630	1	INLB LISMO	P25147 listeria mo	341	87.5	4.8	847	1	R133 ARATH	Q9ste7 arabidopsis
269	95.5	5.2	1027	1	AF10 HUMAN	P55197 homo sapien	342	87.5	4.8	1251	1	YML1 YEAST	Q04545 saccharomyc
270	95.5	5.2	1329	1	KP10 HUMAN	Q9p218 homo sapien	343	87.5	4.8	2594	1	7LIES DROVI	P20806 drosophila
271	95	5.2	463	1	DNAA_PROMP	Q95487 prochloroco	344	87	4.8	659	1	DNAA CHLAB	Q8gh79 chlamydomo
272	95	5.2	593	1	FRZF MYXCA	P31759 myxococcus	345	87	4.8	662	1	GGT4 MOUSE	Q991p7 mus musculus
273	95	5.2	799	1	ZY11 CAEEL	P21541 caenorhabdi	346	87	4.8	699	1	LSHR HUMAN	P22888 homo sapien
274	95	5.2	818	1	TRKB CHICK	Q91987 gallus gall	347	86.5	4.7	1040	1	CARF HUMAN	Q9hc29 homo sapien
275	95	5.2	822	1	TRKB HUMAN	Q16620 homo sapien	348	86.5	4.7	1093	1	NA14 HUMAN	Q86w24 homo sapien
276	95	5.2	901	1	Y298 HUMAN	Q1016 homo sapien	349	86.5	4.7	1155	1	C1HB BACTM	Q45718 bacillus th
277	94.5	5.2	511	1	AL21 SCHPO	Q10303 schizosacch	350	86.5	4.7	2333	1	PGCA CANFA	Q28343 canis fami
278	94.5	5.2	1093	1	AF17 HUMAN	P55198 homo sapien	351	86.5	4.7	2432	1	Y43R IRV6	P18305 chilo iride
279	94	5.1	339	1	FABH STRLI	Q9f6d4 streptomyce	352	86.5	4.7	3341	1	POLG MCFA	P33515 m genome po
280	94	5.1	799	1	TRKA RAT	P35739 rattus norv	353	86	4.7	338	1	DXR_SALUTI	Q829a6 salmonella
281	94	5.1	2258	1	FAS_PIG	Q9glp1 sus scrofa	354	86	4.7	483	1	CTDB HUMAN	Q9h579 homo sapien
282	94	5.1	2717	1	ZEP1 HUMAN	P15822 homo sapien	355	86	4.7	513	1	NORI ALCEU	Q9k4v0 alcaligenes
283	93.5	5.1	677	1	LX1B MOUSE	Q95936 mus musculus	356	86	4.7	556	1	PLD STRAT	Q53728 streptomyce
284	93.5	5.1	1378	1	WP52 ARATH	Q9fh83 arabidopsis	357	86	4.7	926	1	SC24 YEAST	P40482 saccharomyc
285	93	5.1	617	1	SH2 MOUSE	Q9jia7 mus musculus	358	86	4.7	982	1	CELE HUMAN	Q13191 homo sapien
286	92.5	5.1	567	1	PGTA HUMAN	Q92696 homo sapien	359	86	4.7	1157	1	RPOB TROW8	P59642 tropheryma
287	92.5	5.1	837	1	CCR4 YEAST	P31384 saccharomyc	360	86	4.7	1157	1	RPOB TROWH	Q93g22 tropheryma
288	92.5	5.1	1115	1	TBC2 CHLRE	Q8vxp3 chlamydomon	361	86	4.7	2161	1	SKH1 HUMAN	Q9y566 homo sapien
289	92.5	5.1	1776	1	POLR OYV	P20127 ononis yell	362	86	4.7	2161	1	SKH1 HUMAN	P24450 zea mays (m
290	92	5.0	402	1	PGK CHLPN	Q927m5 chlamydia p	363	85.5	4.7	233	1	ZEAD MAIZE	Q63955 mus musculus
291	92	5.0	435	1	CREA BOTCI	Q94130 botrytis ci	364	85.5	4.7	338	1	PO43 MOUSE	P74155 synchocyst
292	92	5.0	481	1	GLNA HELPU	Q921w5 helicobacte	365	85.5	4.7	384	1	OXAA SYN3	Q9h1b4 homo sapien
293	92	5.0	539	1	FXL6 HUMAN	Q8n531 homo sapien	366	85.5	4.7	397	1	NXFS HUMAN	Q9ub9 homo sapien
294	92	5.0	1230	1	UGS4 SOLTU	Q43846 solanum tub	367	85.5	4.7	619	1	NXFL HUMAN	P16582 sus scrofa
295	92	5.0	1372	1	WR16 ARATH	Q9f192 arabidopsis	368	85.5	4.7	696	1	LSHR_PIG	O70494 mus musculus
296	92	5.0	3144	1	VP13 YEAST	Q07878 saccharomyc	369	85.5	4.7	725	1	SP3 MOUSE	Q42484 arabidopsis
297	91.5	5.0	267	1	ZEAX MAIZE	P04698 zea mays (m	370	85.5	4.7	909	1	RPS2 ARATH	O54858 rattus norv
298	91.5	5.0	460	1	VATB THEVO	Q97cp9 thermoplasm	371	85.5	4.7	2254	1	CCAG RAT	Q54858 rattus norv
299	91	5.0	331	1	YB52 SYN3	P74221 synchocyst	372	85	4.6	206	1	GPBB MOUSE	Q9h336 pseudomonas
300	91	5.0	625	1	GCKR HUMAN	Q14397 homo sapien	373	85	4.6	329	1	MOAL_PSEAE	P48313 human adeno
301	91	5.0	781	1	SP3 HUMAN	Q02447 homo sapien	374	85	4.6	646	1	TERM_ADE40	P25017 agrobacteri
302	91	5.0	960	1	PM44 ARATH	Q9su58 arabidopsis	375	85	4.6	755	1	TR2N AGRVI	P76578 escherichia
303	91	5.0	1736	1	CA2B MOUSE	Q64739 mus musculus	376	85	4.6	1653	1	YFHM ECOLI	P27959 pasteurilla
304	90.5	5.0	267	1	KAP2 SORBI	P14691 sorghum bic	377	84.5	4.6	385	1	PAL1 PASMU	Q43959 azotobacter
305	90.5	5.0	469	1	MURD_AGR15	Q8udm6 agrobacteri	378	84.5	4.6	776	1	HYPF_AZOC	P27959 pasteurilla
306	90.5	5.0	567	1	PGTA MOUSE	Q9jhk4 mus musculus	379	84.5	4.6	788	1	BCSB_XANAC	Q58933 xanthomonas
307	90.5	5.0	567	1	PGTA RAT	Q08602 rattus norv	380	84.5	4.6	1895	1	WR19 ARATH	Q9s257 arabidopsis
308	90.5	5.0	852	1	R134 ARATH	Q38834 arabidopsis	381	84.5	4.6	2426	1	SON HUMAN	P18583 homo sapien
309	90.5	5.0	5147	1	FAT DRCME	P33450 drosophila	382	84.5	4.6	267	1	ZEAL MAIZE	P04701 zea mays (m
310	90	4.9	208	1	GPBB PAPCY	Q04785 papio cynoc	383	84	4.6	337	1	PLSX VIBMA	Q9a35 vibrio mari
311	90	4.9	232	1	TRPF_LIPST	Q01128 lipomyces s	384	84	4.6	359	1	KLFB HUMAN	Q95600 homo sapien
312	90	4.9	662	1	GGT4 RAT	Q9sm74 rattus norv	385	84	4.6	481	1	GLNA_HELPY	P94845 helicobacte
313	90	4.9	675	1	HS7M PHAVU	Q01899 phaseolus v	386	84	4.6	538	1	KL11 YEAST	P23291 saccharomyc
314	90	4.9	676	1	LSHR CALWA	Q02721 callithrix	387	84	4.6	580	1	MP12 HUMAN	P30305 homo sapien
315	90	4.9	796	1	TRKA HUMAN	P04629 homo sapien	388	84	4.6	677	1	TKT1 CANAL	Q04039 candida alb
316	90	4.9	1302	1	FRPA NEIMB	Q9k0k9 neisseria m	389	84	4.6	816	1	HDA7 CAEEL	O17323 caenorhabdi
317	90	4.9	1829	1	FRPC NEIMC	Q9jyv5 neisseria m	390	84	4.6	843	1	MNB DROME	P49657 drosophila
318	89.5	4.9	225	1	GIDB THETH	Q9lcy2 thermus the	391	84	4.6	876	1	SIRK ARATH	O64483 arabidopsis
319	89.5	4.9	607	1	YN92 YEAST	P53749 saccharomyc	392	84	4.6	910	1	RP8H ARATH	P59594 arabidopsis
320	89.5	4.9	1025	1	DPD2_PIG	Q28943 sus scrofa	393	84	4.6	2109	1	PGCA CHICK	P07898 gallus gall
321	89	4.9	261	1	ZEAX MAIZE	P08679 zea mays (m	394	84	4.6	2470	1	NCT2 MOUSE	Q35516 mus musculus
322	89	4.9	538	1	YFUL ECOLI	P52127 escherichia	395	84	4.6	2805	1	MAPA HUMAN	P78559 homo sapien
323	89	4.9	1142	1	GIN4 YEAST	Q12263 saccharomyc	396	84	4.6	325	1	Y856 TREPA	O83828 treponema p
324	89	4.9	3707	1	PGBM MOUSE	Q05793 mus musculus	397	83.5	4.6	496	1	MMSA_PSEAE	P28810 pseudomonas
325	89	4.9	3969	1	HRX_HUMAN	Q03164 homo sapien	398	83.5	4.6				

399 83.5 4.6 576 1 SLP1 CAEEL  
400 83.5 4.6 789 1 ATX1 RAT  
401 83.5 4.6 928 1 KRL1 YEAST  
402 83.5 4.6 1162 1 FLB1 HUMAN  
403 83.5 4.6 1204 1 ATY2 HUMAN  
404 83.5 4.6 1592 1 YNY2 YEAST  
405 83.5 4.6 2531 1 NTC1 MOUSE  
406 83 4.5 230 1 ZEA3 MAIZE  
407 83 4.5 344 1 RPOA SPIWK  
408 83 4.5 419 1 GLPB ECOLI  
409 83 4.5 424 1 ARL2 HUMAN  
410 83 4.5 504 1 ARL2 AGRT5  
411 83 4.5 535 1 SRC HUMAN  
412 83 4.5 555 1 FRAA ECOLI  
413 83 4.5 624 1 STS MOUSE  
414 83 4.5 625 1 GLM5 SYNEL  
415 83 4.5 682 1 H87M SOLTU  
416 83 4.5 816 1 NPA2 MOUSE  
417 83 4.5 836 1 VG26 BPML5  
418 83 4.5 2124 1 PGCA RAT  
419 82.5 4.5 326 1 TPO RAT  
420 82.5 4.5 445 1 YB5 MYCTU  
421 82.5 4.5 550 1 LG12 MOUSE  
422 82.5 4.5 585 1 DCP3 ORYSA  
423 82.5 4.5 622 1 FAGC HUMAN  
424 82.5 4.5 628 1 HNP4 MOUSE  
425 82.5 4.5 638 1 HNP4 RAT  
426 82.5 4.5 651 1 TOXA PSEAE  
427 82.5 4.5 824 1 PIA1 MOUSE  
428 82.5 4.5 824 1 NPA2 HUMAN  
429 82.5 4.5 1024 1 S261 HUMAN  
430 82.5 4.5 1033 1 C1S1 MOUSE  
431 82 4.5 304 1 HEN3 XANAC  
432 82 4.5 376 1 AT7 ORYSA  
433 82 4.5 417 1 O85E DROME  
434 82 4.5 437 1 FLHF PSEPU  
435 82 4.5 510 1 HUTH STIAU  
436 82 4.5 535 1 FLX6 MOUSE  
437 82 4.5 540 1 SRC MOUSE  
438 82 4.5 666 1 GGT4 HUMAN  
439 82 4.5 1035 1 MT10 YEAST  
440 82 4.5 1099 1 PLC1 CANAL  
441 82 4.5 1762 1 DPOO HUMAN  
442 81.5 4.5 278 1 PSTB BACHD  
443 81.5 4.5 378 1 SUCC THERH  
444 81.5 4.5 458 1 BPIL HUMAN  
445 81.5 4.5 460 1 VAPB THEAC  
446 81.5 4.5 590 1 ILVB PORPU  
447 81.5 4.5 661 1 Y182 SYN3  
448 81.5 4.5 710 1 DA DROME  
449 81.5 4.5 830 1 JIP2 MOUSE  
450 81.5 4.5 885 1 AR56 SCHPO  
451 81.5 4.5 1070 1 RPOB SP1OL  
452 81.5 4.5 1200 1 ATY2 MOUSE  
453 81.5 4.5 1204 1 POL MLVFF  
454 81.5 4.5 1204 1 POL MLVFF  
455 81.5 4.5 1204 1 MSB6 SCHPO  
456 81.5 4.5 1254 1 EPPL HUMAN  
457 81.5 4.5 5065 1 ZER2 MAIZE  
458 81 4.4 235 1 YMO3 ERWST  
459 81 4.4 295 1 YMO3 ERWST  
460 81 4.4 306 1 PRMA XANAC  
461 81 4.4 377 1 ACTC ARATH  
462 81 4.4 397 1 PGTC SALTU  
463 81 4.4 413 1 COBL PSEDE  
464 81 4.4 455 1 K312 HUMAN  
465 81 4.4 456 1 RINI RAT  
466 81 4.4 460 1 RINI HUMAN  
467 81 4.4 664 1 DNAK CHLCV  
468 81 4.4 700 1 LSHR RAT  
469 81 4.4 704 1 PMA2 LYCES  
470 81 4.4 784 1 OSTA SALTU  
471 81 4.4 2471 1 NTC2 RAT

472 80.5 4.4 477 1 LPC3 HUMAN  
473 80.5 4.4 523 1 SRC RSVPA  
474 80.5 4.4 621 1 ILV5 MYCAV  
475 80.5 4.4 720 1 GT11 SCHPO  
476 80.5 4.4 781 1 YB68 SCHPO  
477 80.5 4.4 811 1 P10A HORU  
478 80.5 4.4 855 1 CLOC MOUSE  
479 80.5 4.4 941 1 MSH1 SCHPO  
480 80.5 4.4 941 1 MSH1 SCHPO  
481 80.5 4.4 1050 1 ULK1 HUMAN  
482 80.5 4.4 1068 1 AF10 MOUSE  
483 80.5 4.4 1155 1 C2TA MOUSE  
484 80.5 4.4 1378 1 RON MOUSE  
485 80.5 4.4 1522 1 ARH1 HUMAN  
486 80.5 4.4 2554 1 7LES DROME  
487 80.5 4.4 4289 1 TENX HUMAN  
488 80 4.4 251 1 A32B HUMAN  
489 80 4.4 304 1 HEM3 XANCP  
490 80 4.4 325 1 THIL ECOLI  
491 80 4.4 399 1 ASSY MYCLE  
492 80 4.4 400 1 DXR PSEPK  
493 80 4.4 424 1 SKP2 MOUSE  
494 80 4.4 476 1 HRA4 HUMAN  
495 80 4.4 531 1 LAC4 THACU  
496 80 4.4 597 1 V70K OVAV  
497 80 4.4 730 1 YE45 SCHPO  
498 80 4.4 943 1 ALB1 MOUSE  
499 80 4.4 1150 1 YC14 SCHPO  
500 80 4.4 1342 1 Z335 HUMAN

## ALIGNMENTS

RESULT 1  
GAMP HUMAN STANDARD; PRT; 713 AA.  
ID GAMP HUMAN  
AC 075325;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Glioma amplified on chromosome 1 protein precursor.  
GN GAC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Glial tumor;  
RC MEDLINE=98324709; PubMed=9662332;  
RA Malfroy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M.,  
RA Dutrillaux A.-M., Dutrillaux B., Ross D., Hanash S.;  
RT "GAC1, a new member of the leucine-rich repeat superfamily on  
RT chromosome band 1q32.1, is amplified and overexpressed in malignant  
RT gliomas.";  
RT Oncogene 16:2997-3002(1998).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: OVERAMPLIFIED IN MALIGNANT GLIOMAS.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -1- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AF030435; AAC39792.1; -  
CC DR MIN; 605492; -  
CC GO; GO:0004872; Fireceptor activity; TAS.  
DR

DR GO: 0007155; P: cell adhesion; TAS.  
DR GO: 0007185; P: signal transduction; TAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_c2.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003591; LRR\_Typ.  
DR Pfam: PF00047; IG\_1.  
DR Pfam: PF00560; LRR; 9.  
DR Pfam: PF01463; LRRCT; 1.  
DR PRINTS: PR00019; LEURICHRPT.  
DR SMART: SM00408; IGC2; 1.  
DR SMART: SM00369; LRR\_Typ; 2.  
DR SMART: SM00082; LRRCT; 1.  
DR SMART: SM00033; LRRNT; 1.  
DR PROSITE: PS00835; IG-LIKE; 1.  
KW Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;  
KW Leucine-rich repeat; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 713  
FT DOMAIN 19 630  
FT TRANSMEM 631 651  
FT DOMAIN 652 713  
FT REPEAT 92 115  
FT REPEAT 116 139  
FT REPEAT 140 163  
FT REPEAT 165 187  
FT REPEAT 188 211  
FT REPEAT 213 235  
FT REPEAT 236 259  
FT REPEAT 261 283  
FT REPEAT 309 333  
FT REPEAT 334 357  
FT REPEAT 359 385  
FT DOMAIN 422 511  
FT DISULFID 445 497  
FT CARBOHYD 94 94  
FT CARBOHYD 381 381  
FT CARBOHYD 555 555  
FT CARBOHYD 583 583  
SQ SEQUENCE 713 AA; 78798 MW; EC8BC0FD240C9396 CRC64;  
Query Match 17.1%; Score 313.5; DB 1; Length 713;  
Best Local Similarity 27.4%; Pred. No. 2.2e-15;  
Matches 114; Conservative 55; Mismatches 162; Indels 85; Gaps 11;  
QY 6 LILLAVSQAQT-----RPCFGCCQCEVTFGLFDSF--SLTRVDCSGLGPHIMPVPI 56  
DB 8 LLLAWAGATAAVPVVPHVCPFCQACQIRPWYTPRSSYREATVDCNDLFLTAVPAL 67  
QY 57 PLDTAHLDLSSNRLMKNESVLVAGPY-TTLAGLDLSNLLTSISPTAFSLRYLESIDL 115  
DB 68 PAGTQTLLQNSIVRVQSEL--GYLANLTLDLSQNSFSDARDCCDFHALPQLLSLHL 124  
QY 116 SHNGTALPAREFTS-SPLSDVNLSHNLRVSVSAFTTHSQGRALHVDLSHNLHRLVP 174  
DB 125 BENQUTRLDISFAGLASLOELYLNHNOQLYRIAPAFGLSNLRLH--LNSNLRAL-- 180  
QY 175 HPTAGLAPAPTQSLNLAWNLRHAY-----PNLRDL----- 205  
DB 181 -DSRFWEMLPNLEILMIGNKVDAILDMNFRPLANRLSVLWAGNLRISDYALEGLQSL 239  
QY 206 -----PLVLSLDGNPLAVIGPGAPAGLGGITLHSLASLQRLP 243  
DB 240 ELSFYDNLQARVPRRALEQVPLGLFDLNNKPLQORVGPGDFANMLHKLGLNNNELV 299  
QY 244 ELAPSGFRELPGQLVLDLSGNPKLNWAGAEVFGSLSLQELDSLSTNLVLPPEALLHL 303  
DB 300 SIDKFAVNLPELTKLDITNNPRLSFHPRAFHLPQMETLMLNNALSALHQQTVESLP 359  
QY 304 ALOSQSV-GQDVRCRLVY-----EGTYPRPGSSPKVPLHCVDTRE 344  
DB 360 NLQEVSLHGNPIRCDVIRWANATGRVRFIEPQSTLCAEPDQLQRLPVREVPFRE 415  
RESULT 2  
GARP\_HUMAN STANDARD; PRT; 662 AA.  
ID GARP\_HUMAN AC Q14392;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE GARP protein precursor (Garpin) (Glycoprotein A repetitions  
DE predominant).  
GN GARP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:94235567; PubMed:8180135;  
RA Ollendorff V., Noguchi T., Delapeyriere O., Birnbaum D.;  
RT "The GARP gene encodes a new member of the family of leucine-rich  
RT repeat-containing proteins.";  
RL Cell Growth Differ. 5:213-219 (1994).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 22 leucine-rich (LRR) repeats.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: Z24680; CAA80847.1; -;  
DR PIR: S42799; S42799.  
DR Genew: HGNC:4161; GARP.  
DR MIM: 137207; -;  
DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003591; LRR\_Typ.  
DR Pfam: PF00560; LRR; 15.  
DR Pfam: PF01462; LRRNT; 1.  
DR PRINTS: PR00019; LEURICHRPT.  
DR SMART: SM00369; LRR\_Typ; 2.  
DR SMART: SM00013; LRRNT; 1.  
DR KW Glycoprotein; Leucine-rich repeat; Repeat; Transmembrane; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 662  
FT DOMAIN 20 627  
FT TRANSMEM 628 648  
FT DOMAIN 649 662  
FT REPEAT 8 31  
FT REPEAT 48 71  
FT REPEAT 72 95  
FT REPEAT 97 122  
FT REPEAT 123 147  
FT REPEAT 148 171  
FT REPEAT 172 195  
FT REPEAT 197 217  
FT REPEAT 218 240  
FT REPEAT 242 264  
FT REPEAT 265 286  
FT REPEAT 314 337  
FT REPEAT 339 361  
FT REPEAT 362 385  
FT REPEAT 386 408  
FT REPEAT 410 432  
FT REPEAT 442 465  
FT REPEAT 467 488  
FT REPEAT 490 513

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FT REPEAT      514      538      LRR 20.
FT REPEAT      540      558      LRR 21.
FT REPEAT      560      583      LRR 22.
FT CARBOHYD    203      203      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    271      271      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    308      308      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    345      345      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    545      545      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE    662 AA; 71978 MW; 700B93ADCDF25960 CRC64;

Query Match      15.3%; Score 279.5; DB 1; Length 662;
Best Local Similarity 28.8%; Pred. No. 6e-13;
Matches 126; Conservative 47; Mismatches 113; Indels 151; Gaps 20;

QY 5 LLLLLAV-----SGAQTTRCPFCQCEVTFGLFDSFSTRVDCSGLGHPHMPVPIPL 58
DQ 5 LLLLLAVLTGLAQHQDKVPC-----KMDVK-----KVSCQVIGLQVPSVLPP 49
QY 59 DTAHLDSSNLEWYNESVLGAP--GYTTLAGLDLSHLLTSIGTAFSRLRYLESDDL 116
DQ 50 DTELDLSGNQL-----RSILASPLGFYALRHLLDLSSTNEISFLOPGAFQALTHLEHLSLA 105
QY 117 HNGL---TALPAESFTSP--LSDVNLSHNQREVSVSAFTTHSQGRALHVDLSHNLHRL 172
DQ 106 HNRALMATAGGLGGLPLPRVTSLDLSGNSLYS-----GLLERL 144
QY 173 VPHPTFRAGLPAPTOSLNLNRLHVAVP--NLRLDLP--LRYLSLDGNPLAVIGPGAFAGLG 229
DQ 145 LGE-----APSLHLSLAENSLRTRTRHTFRDMPALEQDLHSLNVLMDIEDGAFEGLP 197
QY 230 GLTHLSLA-----SLQRL-----PKLNWAGAEV-----PSG- 277
DQ 198 RLTHLNSNSLTCTSDFSLQQLRVLDLSCNSIEAFQSPQAEFQLTWLDLRENKLH 257
QY 243 -PELAPSGFREPLGQLVLDLGN-----PKLNWAGAEV-----PSG- 277
DQ 258 FPDLA-----ALPRLIYLNLSNLRITLTPGPPQDSKGIHAPSEGSALPLSAPSGNASGR 312
QY 278 -LSSQELDLSGTNLVPLPEALLHLPALQSVGVQDVRCLRVREGTYPRPSSPKVP 336
DQ 313 PLSQLINDLSVNETELPDPDFLEHLSLCLFNLNLSRN--CLRTFE-----AARLGLSLFCLM 366
QY 337 L-----HCVDTRESAAR 348
DQ 367 LLDLSHNALETLELGAR 383

RESULT 3
LGR5_HUMAN
ID LGR5_HUMAN STANDARD; PRT; 907 AA.
AC 075473; Q9UP75;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucine-rich repeat-containing G protein-coupled receptor 5 precursor
DE (Orphan G protein-coupled receptor HG38) (G protein-coupled receptor
DE 49).
GN GPR49 OR LGR5 OR GPR67.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98308104; PubMed=9642114;
RA McDonald T., Wang R., Bailey W., Xie G., Chen F., Caskey C.T.,
RA Liu Q.
RT "Identification and cloning of an orphan G protein-coupled receptor of
RT the glycoprotein hormone receptor subfamily."
RL Biochem. Biophys. Res. Commun. 247:266-270(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX
RT TISSUE=Placenta;

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RX MEDLINE=99065210; PubMed=9849958;
RA Hsu S.Y., Liang S.-G., Hsueh A.J.W.;
RT "Characterization of two LGR genes homologous to gonadotropin and
RT thyrotropin receptors with extracellular leucine-rich repeats and a G
RT protein-coupled, seven-transmembrane region."
RL Mol. Endocrinol. 12:1830-1845(1998).
CC -!- FUNCTION: Orphan receptor. It may be an important receptor for
CC signals controlling growth and differentiation of specific
CC embryonic tissues (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in skeletal muscle, placenta, spinal
CC cord, and various region of brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF062006; AAC28019.1; -.
DR EMBL; AF061444; AAC77911.1; -.
DR PIR; JE0176; JE0176.
DR Genew; HGNC:4504; GPR49.
DR MIM; 606667; -.
DR HSP; P23945; LXUN
DR GO; GO:0003887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 14.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_Typ; 8.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
DR G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;
KW Repeat; Leucine-rich repeat.
FT SIGNAL 1 21
FT CHAIN 22 907
FT -----
FT LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-
FT COUPLED RECEPTOR 5
FT EXTRACELLULAR (POTENTIAL).
FT 1 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 2 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 3 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 4 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 5 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 6 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 7 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT LRR 1.
FT LRR 2.
FT LRR 3.
FT LRR 4.
FT LRR 5.
FT LRR 6.
FT LRR 7.
FT LRR 8.

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FT REPEAT 257 279 LRR 9.
FT REPEAT 281 303 LRR 10.
FT REPEAT 304 327 LRR 11.
FT REPEAT 327 350 LRR 12.
FT REPEAT 351 375 LRR 13.
FT REPEAT 377 396 LRR 14.
FT REPEAT 397 420 LRR 15.
FT REPEAT 422 444 LRR 16.
FT REPEAT 444 464 LRR 17.
FT REPEAT 464 485 LRR 18.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 500 500 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 792 792 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 90 90 R -> H (IN REF. 2).
FT CONFLICT 212 212 L -> W (IN REF. 2).
SQ SEQUENCE 907 AA; 99997 MW; 8225C5E6FD9092 CRC64;

Query Match 14.5%; Score 265; DB 1; Length 907;
Best Local Similarity 30.1%; Pred. No. 1e-11;
Matches 93; Conservative 32; Mismatches 102; Indels 82; Gaps 9;

QY 4 PLLLLAVSQAQ-----TTRCFGCGQCEVTFGLFDSFSLTRVDCSGLGPHIMPVPIPL 58
DB 13 PVLLQLATGSGSPRSGLLRGCTHCEP-----DGRMLLRVDCSDGLSELPSNLSV 66
QY 59 DTAHLDSNLEWNEVSLAGPGVTTLAGLDLSHLLTISPTAFGRRLRYLESIDLSHN 118
DB 67 FTSYLDLSNN-----ISQLPNPLSLRFELESLRAGN 100
QY 119 GLTALPASFTS-SPLSDVNLHSHQREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPT 177
DB 101 ALTYPKGFTGLYSLKVLMLQNNQLRHV-----PT 131
QY 178 RAGLPAPTIQSLNLAWEHLHAPVNLRLP-----LRYLSLQCNPLAVIGPGAFAGLG 229
DB 132 BALQNLRLSLQSLRDANHSIVP-----PSCFSGLSLRLHLDLNDALTEIPVQAFRLS 186
QY 230 GITHLSLASLQRLAPLAPSGFRELPGVLQVLDLGNPKLNWAGAEVFGSLSLQELDLSGT 289
DB 187 ALQAMTLA-LNKIHIPDYAFQNLSSLVVLHNN-RHLSKCKGFCGLHSLETLIDLNYN 244
QY 290 NLVPLPEAL 298
DB 245 NLDEFTAI 253

RESULT 4
LGR5_MOUSE STANDARD; PRT; 907 AA.
AC Q921P4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucine-rich repeat-containing G protein-coupled receptor 5 precursor
DE (G protein-coupled receptor 49) (Orphan G protein-coupled receptor
DE FEX).
GN GPR49 OR LGR5 OR FEX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99121227; PubMed=9920770;
RA Hermey G., Methner A., Schaller H.C., Hermans-Borgmeyer I.;
RT "Identification of a novel seven-transmembrane receptor with homology
RT to glycoprotein receptors and its expression in the adult and
RT developing mouse.";
RL Biochem. Biophys. Res. Commun. 254:273-279(1999).
CC -!- FUNCTION: Orphan receptor. It may be an important receptor for
CC signals controlling growth and differentiation of specific

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CC embryonic tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the gonads, the adrenal gland,
CC and in the brain. In the central nervous system expression is
CC restricted to the olfactory bulb. In the adrenal gland detected
CC only in the neural-crest derived chromaffin cells of the
CC medulla, but not in the cells of the adrenal cortex. In the
CC gonads, the expression is high in Graafian follicle, but absent
CC from primary and secondary follicles.
CC -!- DEVELOPMENTAL STAGE: Expressed from embryonic day 10.5 (E10.5) in
CC the developing spinal cord and in the neuroepithelia of the
CC myel-, met-, mes-, and diencephalon. Expression is transitory and
CC the pattern changed rapidly.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
CC
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CC
CC -----
CC EMBL; AF110818; AAD14684.1; -.
CC HSP; P23945; 1XUN.
CC MGD; MG1:1341817; Gpr49.
CC InterPro; IPR000276; GPCR Rhodspn.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00001; 7tm_1; 1.
CC Pfam; PF00560; LRR; 14.
CC Pfam; PF01462; LRRNT; 1.
CC PRINTS; PR00237; GPCR RHODOPSIN.
CC SMART; SM00369; LRR_TYP; 8.
CC SMART; SM00013; LRRNT; 1.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
CC G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;
CC Repeat; Leucine-rich repeat.
CC SIGNAL 1 21
CC CHAIN 22 907
CC LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-
CC COUPLED RECEPTOR 5.
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 22 561
CC TRANSMEM 562 582
CC DOMAIN 583 593
CC TRANSMEM 594 614
CC DOMAIN 615 638
CC TRANSMEM 639 659
CC DOMAIN 660 682
CC TRANSMEM 683 703
CC DOMAIN 704 723
CC TRANSMEM 724 744
CC DOMAIN 745 767
CC TRANSMEM 768 788
CC DOMAIN 789 802
CC TRANSMEM 803 823
CC DOMAIN 824 907
CC REPEAT 64 88
CC REPEAT 89 112
CC REPEAT 113 136
CC REPEAT 137 160
CC REPEAT 162 184
CC REPEAT 186 208
CC REPEAT 209 232
CC REPEAT 233 256
CC REPEAT 257 279
CC REPEAT 281 303
CC REPEAT 304 327
CC REPEAT 328 350
CC REPEAT 351 375

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FT REPEAT 377 396 LRR 14.  
FT REPEAT 397 420 LRR 15.  
FT REPEAT 422 444 LRR 16.  
FT REPEAT 564 585 LRR 17.  
FT CARBOHYD 63 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 792 792 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 907 AA; 99681 MW; 553167C6CAAE253 CRC64;  
  
Query Match 14.1%; Score 257; DB 1; Length 907;  
Best Local Similarity 29.8%; Pred. No. 3.9e-11;  
Matches 89; Conservative 40; Mismatches 104; Indels 66; Gaps 9;  
  
QY 6 LLLAVSAQAQ-----TTTPCPGCOCEVETGLFDSFSLTRVDCSGLGPHMPVPIPLDT 60  
DB 15 LLLAVSAQAQ-----TTTPCPGCOCEVETGLFDSFSLTRVDCSGLGPHMPVPIPLDT 60  
QY 61 AHLDLSSNRLNLEWNSVLGAPGYTTTLAGLDLSHNLTSISPTAFSLRYLESLSLHNGL 120  
DB 69 SYLDLSMNIQSPLASLL-----HRLCFLEELRLAGNAL 102  
QY 121 TALPAESTS-SPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHETRA 179  
DB 103 THIPKGAFTGLSHLKVLMQNLQKRPVEALQNLRLSLQSLRLDANH--ISYVPPS---- 156  
QY 180 GLPAPTIQSLNLAHNLHVNPLRLPLRYLSLDGNPLAVTGPCAFAGLGLTHLSLASL 239  
DB 157 -----CFSGLSH-----LRLHLDNALTDPVQAFSLSLAQAMTLA-L 195  
QY 240 QRLPELAGPRLPGLQVLDSGNPKLNWAGAEVFGSLSLQBELDLSGNTNVLPLPAL 298  
DB 196 NKIHIIADYAFGNLSVLVHLHNN-RHISLKGKCFDGLHSLTLDLNNYNNLDFEPTAI 253  
  
RESULT 5  
LGR4 HUMAN STANDARD; PRT; 951 AA.  
AC LGR4 HUMAN STANDARD; PRT; 951 AA.  
AC Q9BXB1; Q9NYD1;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucine-rich repeat-containing G protein-coupled receptor 4 precursor  
DE (G protein-coupled receptor 48).  
GN GPR48 OR LGR4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=21294803; PubMed=11401528;  
RA Loh E.D., Broussard S.R., Kolakowski L.F. Jr.;  
RT "Molecular characterization of a novel glycoprotein hormone  
G-protein-coupled receptor.";  
RL Biochem. Biophys. Res. Commun. 282:757-764(2001).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in multiple steroidogenic tissues:  
CC placenta, ovary, testis and adrenal. Expressed also in spinal  
CC cord, thyroid, stomach, trachea, heart, pancreas, kidney, prostate  
CC and spleen.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.  
  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF346711; AAK31153.1;  
DR EMBL; AF346709; AAK31153.1; JOINED.  
DR EMBL; AF346710; AAK31153.1; JOINED.  
DR EMBL; AF257182; AAF68989.1;  
DR Genew; HGNC:13299; GPR48.  
DR MIM; 606666;  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR001611; LRR\_Nterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00001; 7tm1.1;  
DR Pfam; PF00560; LRR; 15.  
DR Pfam; PF01462; LRRNT; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR00019; LEUICHRPT.  
DR SMART; SM00369; LRR\_TYP; 4.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00237; G-PROTEIN RECP F1\_1; FALSE\_NEG.  
DR PROSITE; PS00262; G-PROTEIN RECP F1\_2; 1.  
KW G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;  
KW Repeat; Leucine-rich repeat.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 951 LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-  
COUPLED RECEPTOR 4.  
FT DOMAIN 25 544 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 545 565 1 (POTENTIAL).  
FT DOMAIN 566 575 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 576 596 2 (POTENTIAL).  
FT DOMAIN 597 620 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 621 641 3 (POTENTIAL).  
FT DOMAIN 642 661 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 662 682 4 (POTENTIAL).  
FT DOMAIN 683 703 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 704 724 5 (POTENTIAL).  
FT DOMAIN 725 756 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 757 777 6 (POTENTIAL).  
FT DOMAIN 778 783 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 784 804 7 (POTENTIAL).  
FT DOMAIN 805 951 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 55 79 LRR 1.  
FT REPEAT 81 103 LRR 2.  
FT REPEAT 104 127 LRR 3.  
FT REPEAT 128 151 LRR 4.  
FT REPEAT 153 175 LRR 5.  
FT REPEAT 176 199 LRR 6.  
FT REPEAT 201 223 LRR 7.  
FT REPEAT 224 247 LRR 8.  
FT REPEAT 248 270 LRR 9.  
FT REPEAT 272 294 LRR 10.  
FT REPEAT 318 341 LRR 11.  
FT REPEAT 342 366 LRR 12.  
FT REPEAT 368 387 LRR 13.  
FT REPEAT 388 411 LRR 14.  
FT REPEAT 413 435 LRR 15.  
FT DISULFID 618 693 BY SIMILARITY.  
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 505 505 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 292 232 F -> S (IN REF. 1; AAF68989).  
FT CONFLICT 433 433 L -> P (IN REF. 1; AAF68989).  
FT CONFLICT 668 668 L -> S (IN REF. 1; AAF68989).  
SQ SEQUENCE 951 AA; 104460 MW; 5E0C2DFCF22CA1BB CRC64;  
  
Query Match 14.1%; Score 257; DB 1; Length 951;  
Best Local Similarity 25.3%; Pred. No. 4.2e-11;  
Matches 110; Conservative 57; Mismatches 163; Indels 104; Gaps 16;  
  
QY 1 MWPL-----LLLVASGAQTRP--CFPGCOCEVETFGFLFDSFSLTRVDCSGLGPHI 51  
DB 1 MWPLGLLCLFALGULLGSGAGPSGAAPLCAAPCSDGD-----RRVDCSGKGLTA 50

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QY 52 MPVPIPLDTAHLDSLNNRLEWNEVSLAGPGYTTLAGLDLSHNLLTSISPTAFSLRYLE 111
Db 51 VPEGLSAFTQALDISMNNITQLPED--AFKXFPFLEELQAGNDLSFIHPKALSGLKELK 108
QY 112 SLDSHNGLTALPAESTS--SPISDVNLSHNLQREVSVAFTHSQGRALHVDLSHNLH 170
Db 109 VLTQNNQLKTVFSEATRGLSALQSLFDANHTSVPEDSFEGVLQVLR--HLWLDNSLT 166
QY 171 RLVPHPTRAGLPARTIQSLNLAHNLHVP-----NLRDPLRYLSLDGPNLAVIGPGAF 225
Db 167 EVVHPHLS---NLPTQALTLALNKISSIPDFAFTNLSLVV--LHLHNNKIRGLSQHCF 221
QY 226 AGGLGLTHLSLA-----SLQRLPELAPSGFRE-----LPGQLVLDLSG 263
Db 222 DGLDNLETLDLSYNNLGEFFPAIKARPSLKELGFHNSISVIPDGAFTNPLRTIHLVD 281
QY 264 NPKLNWAGAEVFGSLSS-----LQELDLSGTLNVLPLPEAL-- 298
Db 282 NP-LSFVGNFAFNLSLHSLVIRGASMQVQFPNLTGTVHLESUTLTGKISSIPNLCQ 340
QY 299 -----LLHLPALQSVSVGDVRCR-----LVREGTY-----PRPGSSPKVP 336
Db 341 EOKMLRTLDLSYNNIRDLPSFNGCHALEEISLQRNQIVQIKGTFQGLISRLILDSRNL 400
QY 337 LHCVDTRSAARGP 350
Db 401 IHEIHSRAFATLGP 414

RESULT 6
LGR4_RAT
ID LGR4_RAT STANDARD; PRT; 951 AA.
AC Q922H4;
AD 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucine-rich repeat-containing G protein-coupled receptor 4 precursor.
GN GPR48 OR LGR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99065210; PubMed=9849958;
RA Hsu S.Y., Liang S.-G., Hsueh A.J.W.;
RT "Characterization of two LGR genes homologous to gonadotropin and
RT thyrotropin receptors with extracellular leucine-rich repeats and a G
RT protein-coupled, seven-transmembrane region.";
RL Mol. Endocrinol. 12:1830-1845(1998).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AF061443; AAC77910.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR Nterm.
DR InterPro: IPR003591; LRR typ.
DR Pfam: PF00001; 7tm 1; 1.
DR Pfam: PF00560; LRR; 15.
DR Pfam: PF01462; LRRNT; 1.
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PRINTS; PRO0237; GPCRHOOPSN.
PRINTS; PRO0019; LEURICHRPT.
SMART; SM00369; LRR_TYP; 5.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Signal; Glycoprotein;
KW Repeat; Leucine-rich repeat.
FT SIGNAL 1 24
FT CHAIN 25 951
FT DOMAIN 25 544
FT TRANSMEM 545 565
FT DOMAIN 566 575
FT TRANSMEM 576 586
FT DOMAIN 597 619
FT TRANSMEM 620 640
FT DOMAIN 641 661
FT TRANSMEM 662 682
FT DOMAIN 683 703
FT TRANSMEM 704 724
FT DOMAIN 725 756
FT TRANSMEM 757 777
FT DOMAIN 778 783
FT TRANSMEM 784 804
FT DOMAIN 805 951
FT REPEAT 55 79
FT REPEAT 81 103
FT REPEAT 104 127
FT REPEAT 128 151
FT REPEAT 153 175
FT REPEAT 176 199
FT REPEAT 200 223
FT REPEAT 225 247
FT REPEAT 248 270
FT REPEAT 272 294
FT REPEAT 318 341
FT REPEAT 342 366
FT REPEAT 368 387
FT REPEAT 388 411
FT REPEAT 413 435
FT REPEAT 438 461
FT DISULFID 618 693
FT CARBOHYD 68 68
FT CARBOHYD 188 188
FT CARBOHYD 199 199
FT CARBOHYD 294 294
FT CARBOHYD 314 314
FT CARBOHYD 505 505
SQ SEQUENCE 951 AA; 104138 MW; EDD56AC072123461 CRC64;
Query Match 14.0%; Score 256; DB 1; Length 951;
Best Local Similarity 25.9%; Pred. No. 4.9e-11;
Matches 105; Conservative 51; Mismatches 149; Indels 100; Gaps 14;
QY 1 MPWPL-----LILLAVSGAQTRP--CFPGQCEVETFGLPDSFSLTRVDCSGLGPHI 51
Db 1 MPWPLGLLCLFALGLGSGAGSAAFLCAAPCSGDG-----RVDCSGKGLTA 50
QY 52 MPVPIPLDTAHLDSLNNRLEWNEVSLAGPGYTTLAGLDLSHNLLTSISPTAFSLRYLE 111
Db 51 VPEGLSAFTQALDISMNNITQLPED--AFKXFPFLEELQAGNDLSFIHPKALSGLKELK 108
QY 112 SLDSHNGLTALPAESTS--SPISDVNLSHNLQREVSVAFTHSQGRALHVDLSHNLH 170
Db 109 VLTQNNQLKTVFSEATRGLSALQSLFDANHTSVPEDSFEGVLQVLR--HLWLDNSLT 166
QY 171 RLVPHPTRAGLPARTIQSLNLAHNLHVP-----NLRDPLRYLSLDGPNLAVIGPGAF 225
Db 164 SLTEVPVRLSNLPTLQALTLALNKISSIPDFAFTNLSLVV--LHLHNNKIRGLSQHCF 221
QY 226 AGGLGLTHLSL-----ASLQRLPELAPSGFRE-----LPGQLVLDLSG 263
Db 222 DGLDNLETLDLSYNNLGEFFPAIKARPSLKELGFHNSISVIPDGAFTNPLRTIHLVD 281
```

QY 264 NPKLNWAGAEVPSGLSS-----LQELDLSTNLVPLPEAL-- 298  
 DB 282 NP-LSFVGNASPHNLSDLHCLVIRGASLVQVFPNLTGTVHLESITLGTGKISSIPDDLCQ 340  
 QY 299 -----LLHLPALQSVSGQVDCRR-----LVREGTY 325  
 DB 341 NQKMLRTLDLSYNNIRDLPSFNGCFRALEISLQNRNOLIKENTF 385

## RESULT 7

A2GL HUMAN  
 ID A2GL HUMAN STANDARD; PRT; 347 AA.  
 AC P02750; Q96Q24;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucine-rich alpha-2-glycoprotein precursor (LRG).  
 GN LRG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA O'Donnell L.C., Druhan L.J., Avalos B.R.;  
 RA "Molecular characterization and expression analysis of leucine-rich  
 RT alpha-2-glycoprotein, a novel marker of granulocytic  
 RT differentiation."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 36-347.  
 RX MEDLINE=85166241; PubMed=3856868;  
 RA Takahashi N., Takahashi Y., Putnam F.W.;  
 RT "Periodicity of leucine and tandem repetition of a 24-amino acid  
 RT segment in the primary structure of leucine-rich alpha 2-glycoprotein  
 RT of human serum."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1906-1910(1985).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma.  
 CC -!- SIMILARITY: Contains 8 leucine-rich (LRR) repeats.

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DR EMBL; AF403428; AAK95527.1; --  
 DR SWISS-2DPAGE; P02750; HUMAN.  
 DR Siena-2DPAGE; P02750; --  
 DR GO; GO:0016020; C:membrane; NAS.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 8.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00369; LRR\_TYP; 4.  
 DR SMART; SM00082; LRRCT; 1.  
 KW Plasma; Glycoprotein; Repeat; Leucine-rich repeat; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 347 LEUCINE-RICH ALPHA-2-GLYCOPROTEIN.  
 FT REPEAT 91 114 LRR 1.  
 FT REPEAT 115 138 LRR 2.  
 FT REPEAT 140 162 LRR 3.  
 FT REPEAT 163 186 LRR 4.  
 FT REPEAT 188 210 LRR 5.  
 FT REPEAT 212 234 LRR 6.  
 FT REPEAT 235 258 LRR 7.  
 FT REPEAT 259 282 LRR 8.

FT DISULFID 43 56  
 FT DISULFID 303 329  
 FT CARBOHYD 37 37 O-LINKED  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 347 AA; 38178 MW; 20C99ED50152FA9C CRC64;

Query Match 13.6%; Score 248; DB 1; Length 347;

Best Local Similarity 33.0%; Pred. No. 5.2e-11;  
 Matches 106; Conservative 34; Mismatches 117; Indels 64; Gaps 16;

QY 5 LLLLLAVSG-AQTRPCFCQCEVETFGLPDSFSLTRVDCSGLGPHIMPVPIPLDTAHL 63  
 DB 25 LLLLLAASAWGVTLSF--KDCQ-----VFPSDHGSSISCO--PFAEIPGVLPADTVHL 73  
 QY 64 DLSSNLEMNESVLAPGYTTIAGLDLSHNLTSISPTAFSRRLRYLESLSLHSHGLTAL 123  
 DB 74 AVEFFNLTLPANLLQGA--SKQLHLHSSNGLESLSPEFLAPVQLRAVLDLTRNALTGL 131  
 QY 124 PAESF-TSSPLSDVNLHNLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTAGLP 182  
 DB 132 PFGLFQASATLDTLVLENQLEVLVS--WLHGLKALGHLDLSGNRLKLP-----GIL 184  
 QY 183 A--PTIQSNLANWRLHVPN--LR-DLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLA 237  
 DB 185 ANFTLRLTLDLGENQLETLPDLRLRGPQLQERLHLEGNKQLVGLKDLL----- 232  
 QY 238 SLQRLELAPSGFRELPGLQVLDLSGNPKLNWAGAEVPSGLSSLQELDLSTNLVPLPEA 297  
 DB 233 ----LPQ-----PDLRYLFLNGN-KLARVAAGAFQGLRQDLMDLSNNSLASVPEG 278  
 QY 298 LILLHLPALQSVSGQ---DVR 315  
 DB 279 LW-----ASLGQPNWDMR 291

## RESULT 8

GPV HUMAN  
 ID GPV HUMAN STANDARD; PRT; 560 AA.  
 AC P40197;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Platelet glycoprotein V precursor (GPV) (CD42D).  
 GN GP5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=93391348; PubMed=7690959;  
 RA Hickey M.J., Hagen F.S., Yagi M., Roth G.J.;  
 RT "Human platelet glycoprotein V: characterization of the polypeptide  
 RT and the related Ib-V-IX receptor system of adhesive, leucine-rich  
 RT glycoproteins."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8327-8331(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Platelet;  
 RX MEDLINE=94012616; PubMed=8407908;  
 RA Lanza F., Morales M., de la Salle C., Cazenave J.-P., Clemençon K.J.,  
 RA Shimomura T., Phillips D.R.;  
 RT "Cloning and characterization of the gene encoding the human platelet  
 RT glycoprotein V. A member of the leucine-rich glycoprotein family  
 RT cleaved during thrombin-induced platelet activation."  
 RL J. Biol. Chem. 268:20801-20807(1993).  
 RN [3]  
 RP PARTIAL SEQUENCE.